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OM nucleic - nucleic search, using sw model

Run on: December 9, 2002, 21:13:58 ; Search time 167 seconds  
(without alignments)  
9549.217 Million cell updates/sec

Title: US-08-978-277A-3

Perfect score: 5200

Sequence: 1 ATGGGCGCAGGAGATTCCAC.....CAGGGCGCTCCAGATTTC 5200

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_NA:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3903.4	75.1	5134	2	US-08-635-121-1
2	1920	36.9	6605	1	US-08-769-309A-4
3	1920	36.9	6605	3	US-08-994-570-4
4	99.8	1.9	7218	1	US-08-232-463-14
5	71.2	1.4	1926	4	US-09-249-585A-4
6	71.2	1.4	1931	2	US-09-130-114-2
7	70.8	1.4	1926	4	US-09-249-585A-2
8	70.8	1.4	2280	3	US-09-050-863-2
9	70.8	1.4	2580	4	US-09-359-081-2
10	70.8	1.4	5452	2	US-09-130-114-1
11	70.8	1.4	9600	4	US-08-910-647-1
12	70.8	1.4	9600	4	US-09-620-925-1
13	70.8	1.4	10596	1	US-07-884-811-15
14	70.8	1.4	10596	1	US-07-885-971-15
15	70.8	1.4	10596	1	US-08-087-783A-15
16	70.8	1.4	10596	1	US-08-194-088B-15
17	70.8	1.4	10596	2	US-08-194-087-15
18	70.8	1.4	10596	5	PCT-US93-04648-15
19	66.4	1.3	3489	2	US-08-728-323A-1
20	66.4	1.3	3489	4	US-09-298-568-1
21	66.4	1.3	32207	2	US-08-770-379-20
22	66.4	1.3	32207	4	US-08-757-669A-20
23	66.4	1.3	32207	4	US-09-230-371A-20
24	64.6	1.2	16442	3	US-08-781-891-208
25	60.4	1.2	2277	1	US-08-676-967-2
26	60.4	1.2	2277	1	US-08-676-974-2
27	60.4	1.2	2277	2	US-09-098-487-2

28	60.2	1.2	3337	1	US-08-072-610-1	Sequence 1, Appl
29	60.2	1.2	3337	2	US-08-719-822B-1	Sequence 1, Appl
30	60.2	1.2	3337	4	US-09-092-458-1	Sequence 1, Appl
31	58.8	1.1	51259	1	US-08-781-891-209	Sequence 209, App
32	56.4	1.1	3211	2	US-08-574-959A-8	Sequence 8, Appl
33	56.4	1.1	3211	4	US-09-357-014-8	Sequence 6, Appl
34	56.4	1.1	3901	4	US-08-574-959A-6	Sequence 6, Appl
35	56.4	1.1	3901	4	US-09-357-014-6	Sequence 1, Appl
36	55	1.1	1052	1	US-08-466-603-1	Sequence 1, Appl
37	55	1.1	1052	1	US-08-314-503A-1	Sequence 1, Appl
38	55	1.1	1052	1	US-08-468-066-1	Sequence 1, Appl
39	55	1.1	1052	2	US-08-466-717-1	Sequence 1, Appl
40	55	1.1	1052	5	US-08-466-743-1	Sequence 1, Appl
41	55	1.1	1052	5	PCT-US95-12414-1	Sequence 1, Appl
42	52.6	1.0	1505	3	US-07-915-246-1	Sequence 101, App
43	51.8	1.0	43795	3	US-08-742-185-101	Sequence 3, Appl
44	47.8	0.9	2518	4	US-09-433-699-3	Sequence 2, Appl
45	47.6	0.9	1276	4	US-09-177-325-2	Sequence 2, Appl

## ALIGNMENTS

RESULT 1  
US-08-635-121-1  
; Sequence 1, Application US/08635121  
; Patent No. 5910442  
GENERAL INFORMATION:  
; APPLICANT: Gelman, Irwin H.  
; TITLE OF INVENTION: TUMOR SUPPRESSOR GENE  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond  
; STREET: 30 Rockefeller Plaza  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10112-0228  
COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
; CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/635,121  
; FILING DATE: 19-APRIL-1996  
CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
; FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
; NAME: Clark, Richard S.  
; REGISTRATION NUMBER: 26,154  
; REFERENCE/DOCKET NUMBER: A30558 - 165/33603  
TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-408-2558  
; TELEFAX: 212-765-2519  
TELEX:  
; INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
; LENGTH: 5134 base pairs  
; TYPE: nucleic acid  
STRANDEDNESS: single  
; TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
FRAGMENT TYPE:  
; ORIGINAL SOURCE:  
US-08-635-121-1  
Query Match 75.1%; Score 3903.4; DB 2; Length 5134;  
Best Local Similarity 97.5%; Pred. No. 0;



3134 GGTCAAAAGCACTGGAGAAAGCTTTGAGAGGTAGAGAGAGCACTCCGAAGTCTGCTTCGG 3193  
2148 GGTCAAAAGCACTGGAGAAAGCTTTGAGAGGTAGAGAGAGCACTCCGAAGTCTGCTTCGG 2207  
3194 AGAAAGAAAGAGAGCTTTATGCCCCAAAGAGACCTGCGAGAGAGTGGAGCTGAGACTTTG 3253  
2208 AGAAAGAAAGAGAGCTTTATGCCAAAGAGACCTGCGAGAGAGTGGAGCTGAGACTTTG 2267  
3254 CAGAGGCTCTGAGACTGGAGAGCTACTCCAGAGAGCTTTGAAGTTCCGAGTCAAG 3313  
2268 CACAGGCTCTGAGACTGGAGAGCTACTCCAGAGAGCTTTGAAGTTCCGAGTCAAG 2327  
3314 CAGATGTAGACATGTGCGCCAGCTGCGAGTTATCAAGTCCAGAGCTGATGGAACAGG 3373  
2328 CAGATGTAGACATGTGCGCCAGCTGCGAGTTATCAAGTCCAGAGCTGATGGAACAGG 2387  
3374 CCGTGGCCCCGTGAGTATCCGAAACCTTGACACACAGTGAACAAATGGAGCACTCCCT 3433  
2388 CCGTGGCCCCGTGAGTATCCGAAACCTTGACACACAGTGAACAAATGGAGCACTCCCT 2447  
3434 TACAGATTTAGACATGTGCGAGTGGGACACAGAGATGAACCATTTGACAGCAGGACA 3493  
2448 TACAGATTTAGACATGTGCGAGTGGGACACAGAGATGAACCATTTGACAGCAGGACA 2507  
3494 GTAAAGCCACTGAGCTGTGAGGAGTCAAGAGTCAAGAGAGAGAGCGGCTACTGCTC 3553  
2508 GTAAAGCCACTGAGCTGTGAGGAGTCAAGAGTCAAGAGAGAGAGCGGCTACTGCTC 2567  
3554 AGAAAGAGAGCTTTGAGCACTACTATATATTTCCAGCCCAAGAGAAACATGGGGAG 3613  
2568 AGAAAGAGAGCTTTGAGCACTACTATATATTTCCAGCCCAAGAGAAACATGGGGAG 2627  
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2628 AACGAGAGAGATGTTCTTGAACCTACACAGAGAGCTTACTGCTGAGCGGCTGCGG 2687  
3674 TTTCTGCAAAAGACTGAGTGGGCTCAAGAGGAGTGAAGTGAAGTGGTGGATGAGAAAAA 3733  
2688 TTTCTGCAAAAGACTGAGTGGGCTCAAGAGGAGTGAAGTGAAGTGGTGGATGAGAAAAA 2747  
3734 TCAGAGAGAGAGAGAGTGTGTTGACCTCTGAGACCTCAAGAGCTGAGTGTGATG 3793  
2748 TCAGAGAGAGAGAGAGTGTGTTGACCTCTGAGACCTCAAGAGCTGAGTGTGATG 2807  
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2928 AGCAAAAGCAGAGAGAGTGTGTTGACCTCTGAGACCTCAAGAGCTGAGTGTGATG 2987  
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3108 AGTTTCAAGTTCAGAGAGCTGAGACACAGTCACTCAAAAGAGAGAGAGTGTGATG 3167  
4154 TCATAGAAAGCGTTGATTTGAGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4213  
3168 TCATAGAAAGCGTTGATTTGAGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3227  
4214 TATTACAGCTGAGAGAGTCTCTGCAAGCGGTGGCAGCTTTCAGCATGAGAG 4273

3228 TATTACAGCTGAGAGAGTCTCTGCAAGCGGTGGCCAGTGAAGTTCAGCATGAGAG 3287  
4274 ACAGGTTACCCCTGGGGGCTGAGTCTCAGGAGAGATCCATCCATCATATGTAAGTCTG 4333  
3288 ACAGGTTACCCCTGGGGGCTGAGTCTCAGGAGAGATCCATCCATCATATGTAAGTCTG 3347  
4334 CTCCTGAAGAGAGAGTCAATCTGAGCTGACATCAAGAGAGAGTGAAGTGAAGTGAAG 4393  
3348 CTCCTGAAGAGAGAGTCAATCTGAGCTGACATCAAGAGAGAGTGAAGTGAAGTGAAG 3407  
4394 GATCAG 4453  
3408 GATCAG 3467  
4454 CAATGCAAAAGTCTTCAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4513  
3468 CAATGCAAAAGTCTTCAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3527  
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4574 CCGAAATCATGCTTTATGATTCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4633  
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3648 AGCCCAAGAGAGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3707  
4694 CAGAGAGAGAGTCTGAG 4753  
3708 CAGAGAGAGAGTCTGAG 3765  
4754 TGCAGGCTGCTGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4813  
3766 TGCAGGCTGCTGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3825  
4814 ACCCAAGAGTCCAAAG 4873  
3826 ACCCAAGAGTCCAAAG 3884  
4874 CAGAGAGAGAGTCTGAG 4933  
3885 CAGAGAGTCTGAG 3941  
4934 TAAACGAG 4993  
3942 TAAACGAG 4000  
4994 CAGTCAAG 5053  
4001 CAGTCAAG 4060  
5054 CAGATCTCAAG 5113  
4061 CAGATCTCAAG 4120  
5114 TCACAG 5173  
4121 TCACAG 4179  
5174 CAG 5200  
4180 CAG 4206

RESULT 2  
US-08-769-309A-4  
; Sequence 4, Application US/08769309A  
; Patent No. 5741890  
; GENERAL INFORMATION:





[illegible]

D	2724	GTGTCCCTCTGTGTGATATGATGCTGTGAAAGGAGAAATGAGGACACGACGAC	2783
Q	2536	CAGGGGAATTACGAGCGTCCCAAGCTGCTGGGGGCTGTGTAGTGTCCGAGAGCTCAGT	2595
D	2784	CAAAAAGGCCGAGAGACGCCCGAGAGAGGACGACGACCTGAGGTGTCCAAAGAGCTCAGC	2843
Q	2556	AAGACTGTGTTCCACTGTGAGTGTGCGACTATTGATGGACACAGGCGACTCACAGT	2655
D	2844	GAGAGTCAGGTTCAATATGATGGCAGCAGCTGTGCTGACGGGACGAGGGCAGCTACATT	2903
Q	2656	GTCGAAGGCGGTCTCTTGTTGGATATCCGCTTCCGTAAACAAACTTTGAACACACA	2715
D	2904	ATTGAAAGAAAGTCTCTCTTGTGGATATGCTTTCAGTACAGAACTCTTGTAAACAACTA	2963
Q	2716	GCGGGAGAGGCATGACCACTGTGTTGAAGAGTACAGTAAAGAAACATCATCTTCG---	AGAA 2772
D	2964	GAACCTGAAGCCGACACTGTTAACTGAGAGAGTATTGGAAAGAAAGTAATTTCCAGAAACA	3023
Q	2773	GAAACTCTGTGCTCACCCAGACGTTACAGAGGGTTAAAGATGCCCATGACACATGGTC	2832
D	3024	GAACCCCCACGGTTACTGAACCTGTCCGAGAAACAGAGAGGCCGGGGCGACACGGTC	3083
Q	2833	ACCAAGTAAGTGATTTCCACTCAGAAAGCTGTGACAGCCACAGAGACCTCAGAGGCTTC	2892
D	3084	GTTAGTGAAGGGGATTTGACCCCGGAAGCTGTACAGCTCAGAAACTGTCCAGGGCCATTG	3143
Q	2893	CGTACTGAAGAGTTTACCAGAACATCGGGGGCCGGAAGACACACAGACATGTGTGCCCA	2952
D	3144	GTTTCCGAAGAGAACCCGAAGCATCTGCTGCTGAAGAGAACCCAGAAATGGTGTACACA	3203
Q	2953	GTTTCCAGCTGACTGACTCCCGACACACAGAGAAAGCCACCCAGTTTCAGAGAGTA	3012
D	3204	GTTCCAGTTAAACGCATCCCGACACACAGAGAGAGGACATCCGGTGAAGAGGTG	3263
Q	3013	GAGAGTGTGTGCTACGATTAAGAAAGAGAGAGCCACACCCAGGCACTCTCCAAACC	3072
D	3264	GAAGGTGGCGTACTGTGCATTAAGAAAGACAAAGAGGCGGACATCAAGAGGTCTCCAGACA	3323
Q	3073	GTTCCAGACAGGTGAAGAGAGAGTCCAGAGTCCCTGCACAC---	CAGACTGTGCAGGA 3129
D	3324	GTTGCCAGAAAAGTGAAGAGAGATCCACAGTCTGTCGACCGGTGGGCCAGAGATGTG	3383
Q	3130	ACGGGGGTCAAAAAGCACTGAGAAAGATTGAGAGAGTGAAGAGAGTCCGAAGTGTGCT	3189
D	3384	CTTCAGCCTGTGCAGAGAGGACAGAGGACAAAGACCAAGAGACAGAGGTGAAGCGTGGGT	3443
Q	3180	TCGGAGAAAGAGAAAGACGTTATATCCGAAAGACCCGCTCAGAAAGCTGTGAGCTGAGAT	3249
D	3444	CTGAAGAAAGAGAGGATGTATGTGTTGAAGTATGATGCTCAGAGAGGCAAAAATGAGCGCT	3503
Q	3250	CTTCCACAGGGCTGTGAGTGTGACAGAGGCTACCCAGAGGCTTG---	AAGTCTCTCAA 3306
D	3504	TTTACACAGAGGAAGGTGTGGGGCAGACACCAGAAAGCTTTGAAAAAGCTTCTCAA	3533
Q	3307	GTCACGGCGAGTGTATGTA-----	GACCAATGTGCCACCTGCGCA----- 3341
D	3564	GTCACAGAGAGCATATAGAGTCCAGTGAAGCTTTTAACCACTGTGTCAAGCGGAAACCTTACT	3623
Q	3342	--GGTTATCAAGCTCCAGCAGCTGATGAAACAGGCCGCTGGCCCTGTAGTACTCGAANAC	3399
D	3624	GGGGTAAATATCACAGGAGATGTGATGGAACAGGCTATCTCCCTGTAGCTCGGTGGAAACC	3683
Q	3400	TTGACAGACGTGTGACAAATGTGAAGCACCTCCCTTATGACGATTCAGACACTGTGAGATGGG	3459
D	3684	CTTACACACGTGTGATGTGGAACACCCCGTATGCGACTTTGTAGCAGCACACAGGCACA	3743
Q	3460	ACACAGCAAGATGAACCATTTGACACCCAGACAGTAAAGCCACTGTACAGCTGTCAAGCAG	3519
D	3744	ACCCAGAAAGCGAGATTTGGAAATTCATAGAGAGAAATGAG---	GTGCATCTGTGTACA 3800
Q	3520	TCACAGGTCAACAGAAAGAGCGGCTACTGCTCAGAAAGAGAGACCTTTCACACACTACT	3579
D	3801	GTTCAGGGGCGACAGAGAGAGGAGTCTCTGTGCACAGAAAGAGAGGCTCTCCAGAGACTTCC	3860



Db 432 CTAAATGCCAGAAAGAGCCCTGAACGGTCAAGAGCCCTAAACAGCCAGAGAGAA 491  
QY 247 GAAGTGTGATGAGATGTTGGACAGCCAGATCAGAAAGATTTGAGAAAAAGCCGA 306  
Db 492 GAAGTATTGTACGAGAGGTTGGACAGAGACTCTGAAGATGTGACGAAGAAGCTCC 551  
QY 307 GTTGAAGAAATGCGCGCCAACTCCACAGCTTGGAAGATTCACAAAGATGGCGAGAG 386  
Db 552 GATAAAGATATGCTACTAATGATCAGCGGTTGTTACAGACATCCAAATGATGGCGAGAG 611  
QY 367 GAGACATCAGAAATTAATGAACAGATCCCTGCTTGAAGAAAAACAATGTGGAAGAAATGTA 426  
Db 612 GAGA---ACCGAAATATCAACAGATTCCTCTTCAGAAAGCAATTAAGAGAGTAA 668  
QY 427 CAGCCTGTCAGTCCAGCTATATGATGTTGGCTTCAAGAAAGTATTTAATTTGTTGGT 486  
Db 669 CAACCCATGAGTCCAGGCTAATGATATTGATTAAGAAAGGTATTGAATTTGTTGGC 728  
QY 487 TTTAAATTCAGGTGAAGAGATTAATAAATGAATAAGTACAGATCTGCCAATCTACAT 546  
Db 729 TTTAAATTCATCTGTGAAAAAGATTAAGACAGAGAACCTGACATCTCCAGCTACTACT 788  
QY 547 GTCAAGAGATGTAAGCGCAAGGGGCGAAGAGCCTCTGTGAGAGCTGAGACCAAGAG 606  
Db 789 GTGAAGAAAGATGTAAGGGGAGGAGCGAGCA-----GGGGCTGGCGACCAAGAGAC 839  
QY 607 CCCAGTGTGAGACTCCCTCGGAGAGTCAAGCATCCAAAGAAAGTGAAGCTGAAGCAATCC 666  
Db 840 CCCAGCTTTGGGGCT-----GGAGAGCAAGCATCCAAAGAAAGCAACCAACATCT 893  
QY 667 ACAGAGAACCAAGAGAGCAACCTGAAGCAAGACAGAGAGCAAGAAATCCCTTTCAA 726  
Db 894 ACAGAGAAACCGGAAGAGACCTGGAAGCGTGAAGCAAAAGCCAGCAAAATTTCTCCCA 953  
QY 727 GCCGAATCTGATCAGCGCTGAGAAAGAACCAAGATGAAGAGAGAGAAAAACAAGAG 786  
Db 954 GCCGAATCTGGCCAA---GCAGTGAAGATGCAAAAGAGAAAGAGAAAGAGAAACAAGAA 1010  
QY 787 AAAGAGCCCAACCAAGTCCCGAGATCCCGAGAGCCCAAGTCAACGTAGACAAACATCT 846  
Db 1011 AAAGAACTTAGCAAGTCTGAGAGATCTCCGACTAGTCCGTGACCAAGTGAACAGAGATCA 1070  
QY 847 TCCCTTCAAGAGTTCTTCACTACAGGTTGGCGGCTGGCGCAAGAGACACAGCTTCAAG 906  
Db 1071 ACCTTCAAAAATTTCTTCACTCAAGSTTGGCGGCTGGCGCAAAAAGACAGCTTTCAGG 1130  
QY 907 AAATCAAAAAGAGATGATCTGAAACTGCCGAGAGAGAGAAAGGCAAGAGCGAGAAAAA 966  
Db 1131 AAGCCGAAGAGGATGATGATGAAAGCTTCAGAGAAAGAAAGAAAGCAAGAGCGAGAAAAA 1190  
QY 967 GTAGACGAGGAAGAAAGAAAGAAAGACAGAGCCAGCTCCGAGAG----- 1010  
Db 1191 GTAGACAGAAAGAGAAAGAAAGAGAGAGTTGCTCCGAGAAACTGACCGCTCCGAG 1250  
QY 1011 -----GCAGAGCCCGGCGAGAAAGACACAGACAGAGCCAGTTGTTCAGAGACTAC 1059  
Db 1251 CAAGCCCAACCCAGSAGGCGGCGAGAAAGTGCACACAGAGCCCGGTTATTCAGTGAATAT 1310  
QY 1060 GAGAGAGTGGAGCTGCTTTTGGAAAGACAGGTTGTGATCCTGGAGGCATCTGTCAGAGAG 1119  
Db 1311 GAGAAAGTTGAGCTGCCCTCAGAGGAGCAAGTCAATGCTCGAGAGACCTTCTGAAGAG 1370  
QY 1120 AAGTGTGCTCTTTGGCAAGGAGTGTGATGAAATGGAATGGAACCCACCAAGAA--- 1176  
Db 1371 AAACCTGCTCCGTGGCAGACAGAGTTTGAAGAGAAATTAAGATTCACCAAGAGAG 1430  
QY 1177 GTTGTGACAGAGTCCACGTGACACCGTGGAGAGACAGAGAGGAGAGGAGAGAGAGA 1236  
Db 1431 GTTGTGCGGAGAGTCCAGCTCAGACACCGTGGAGAGAGAAACGAAGAGAGAGAAAC----- 1486  
QY 1237 GGAGAGGCTGAAGGGGCGTGTGTGAGAGAAAGAGAAATCTTGTCCCTCGAGAAA 1296  
Db 1487 -----GGAGGTGGAAGAAACAGAGGCTGTGTGCCAGCTGAAGAA 1526

QY 1297 CTGGCTGAGCCCGAGAGGTTCCCGAGAAAGCTGACGCTGCTGAGAGGCTGATGAAGAGC 1356  
Db 1527 TTGTTGGAATGAGATCAGAACTCAGAGAGCCGAACCTGCAAGAGCTGGGAGAGCTC 1586  
QY 1357 AGAGAGATGTGTCTCTGAGAGAGACCACTCACTGACAGAGCTTAAGTCTCGAAGAG 1416  
Db 1587 AAGAAAGCTGTGTTTCCGAGAGAGACCTTACACAGAGAGCTACCTCAAGTCTGATTGAG 1646  
QY 1417 AAGACCTGCCCAACACCCAGAGAGCATTTGTCAATGAGGTGAGATGCTGTCTCTCAG 1476  
Db 1647 AAGTGTCTGTCAAACCCCGAAGCGGTTGTGATGAGAGGTGAATGCTGTCATCAGAG 1706  
QY 1477 GAAAGATCAAGGTACAGGAAGTCCCTTGAAGAAACTCTTCAGTAGCTCAGGCTTAAAG 1536  
Db 1707 GAGAGATGAAGGTGAGGGAAGTCACTAAACCTTTTAAACAGCACTGGCTTAAAA 1766  
QY 1537 AAGCTGTGGGAAGAGAGAGAGGGAAGAGAGAGGTGGGAGAGACGAAGAGCTTGA 1596  
Db 1767 AAGCTTTCTGGAAGAAAGAGAGAGGAAAAAGAG---GAGAGACACAGAAATCAGG 1823  
QY 1597 GAATCCAAACATTTCACACCGAATCCCAAGAGATGCTGATGAGCAAGAGAGAGAGAC 1656  
Db 1824 GAGCAACTCAGGTTCCAGCCGATTTCTCCGACAGCAAGAGAGCAAAAAGGCGAGAGC 1883  
QY 1657 TCTGCGTCCGCCCCGAGAGCCTGAGAGACCACTGTCTGAGAAAGAGCCGCTGGA 1716  
Db 1884 TCTGCTCATCTCCCTGAGAGCCGAGAGATCACGTGCTGGAAGAGGCTTAAGCCGAG 1943  
QY 1717 GCACCCAGAGATGGGAGAGCTGAGAGAGAACTACTTCCGATGAGAGAGAAAGAGAGAA 1776  
Db 1944 GTCCACAGAGATGGGAGAGCTGAAGAGAGAGTACTTCCGATGAGAGAGAAAAAGAGAA 2003  
QY 1777 GGGATCACTCCCTGGCATCTTCAAAAAGATGTGACACCCAAAGACGGGTCCAGAA 1836  
Db 2004 GGTGTCACTCCCTGGGCATCATTCAAAAAGATGTGACCCCAAGAGGCTGTTAAGACGG 2063  
QY 1837 CCTTCTGAGGTGACAAGGGGAGAGCTGGAGAAAGTCAAGAGGCCCACTGTGCTCC 1896  
Db 2064 CTTTGGAAAGATATGAAGATGAGCTGGACAAAGTCAAGAGCCCTACCTTGTCTCC 2123  
QY 1897 ACTGATGACACAGTCTCAGAAATGCAAGATGAAGTCAAAACTTTGGTGAAGAAACAAAG 1956  
Db 2124 ACCGAGAGGACACCTCTGAATGCAAGAAAGAAATGAAGGGAGCGTGAAGAGCCAAAG 2183  
QY 1957 CCAGAGAGCAAAAGCGTAGGTGATPACTTCACTGTCTTGGAGACACTGATTTGTCTC 2016  
Db 2184 CCGGAGAGAAACCAAGCGCAAGGTGATACCTCAGTATCTTGGGAACCTTAAATTTGTGTG 2243  
QY 2017 GATTCATCCAAAGAGAGAGCAAGAGGCACTCTTTCAGATGATGAAGAGGCGCAAGG 2076  
Db 2244 GATTCATCCAAAGAAAGAGCAAGAGAGGCTCTTCTGATGAGAGGGGACCAAAA 2303  
QY 2077 ACACCTGGAGGGAGACAGTACAGAGAGAGAGAGGACAGCAAAAGACAAAGCCGAGACA 2136  
Db 2304 GCATGTGGAGAGAGACACCAAGAAAGCTGATGAGAGCGCGGAAGAAACAAAGAGAGGGGACA 2363  
QY 2137 GACGCTTCTCTGCAAGACCAAGAGACAGAGCAAGCGCAAGAGATTCTCACCCGAG 2196  
Db 2364 GACGGATCTCTGCTGTTTCCCAAGAACATGATCCAGGCGAGGAGAGTCTCTCCCGAG 2423  
QY 2197 CCAAGGGGAAGCCCTTCCAAAGGGGAAGGTGTCCTCACTTGGAGATCTTAAAGATTA 2256  
Db 2424 CAAGCTGGAAGCCCTTACCAAGGGGAGGCGTTTCCACTGGGAGTCAATTTAAAGATTA 2483  
QY 2257 GTCACTCCAAAGAAAAATCCAAAGTGAAGAGAGAGAAAGCCGAGAAC----- 2307  
Db 2484 GTCAAGCCAAAGAAAAATTCAAAGTCCAAAGCTGGAAGAGAGAAAGCAAGACATCCATAGCT 2543  
QY 2308 ---TCTAGTGTAGAGCATGTTGCTCACTGATGAAACGAGTAGAGAGAAATCTTGGGTT 2364  
Db 2544 GGCTGTGTTGATGAACTTCACACTCCAGACACTGAAACCGGTAAAGAAATCTGTGGTTC 2603

OY	2365	TCCATTGAAGAAATTCATCTCGGACGGCGGAAAGAAAAGGCCAGAGGGGAAAGCAACA	2424
Db	2604	TCAAATCAGAAGTTTATTTCTTGCGAAGAGAAAAAGCCAGATGGGAAACAGAACAA	2663
OY	2425	GCCACTGTGGAAGACACAGGCGCAGTAGAGATAAATGAGAGCACGCCTTATGTCCAGACC	2484
Db	2664	GGCCCTGTGAAGAGCCAGGCCCCAACAGGGGCCAACAGSAGATGACTGTATGTCCCAGCC	2723
OY	2485	GTCGTGCTCTGTCTGAGATTAATGCAAGTGAGAGGGGAGAAGATGG-----AAGCC	2535
Db	2724	GTGTGCCCTCTCTGTGATGATGCTGTAGAAGGGAGAAAAATGAGAGGCACAGCAAGCC	2783
OY	2536	CAGGGGAATACGGAGCTGCCCAAGCTGCTGGGGCTGTGACTGTCCGAGGAGCTACGT	2595
Db	2784	CAAAAAGCGCAGAGAGAGCCCGCAGCAAGGAGCCCATGAGGTGTCCAAGGAGCTCAGC	2843
OY	2596	AAGACTCTGTCCACACTGTGAGTGTCCGAGTATGATGGACAGGGCAGTACACAGT	2655
Db	2844	GAGAGTCAGGTTTCATATATGATGGCAGCAGCTGTGCTGACGGGACGAGGGCAGCTTACCATT	2903
OY	2656	GTCCGAAGACGGCTTCTCTTGATATCCGCTTCCGTAACAGAACCTTTGAACACACA	2715
Db	2904	ATTGAAGAAAGGCTCTCTTGATATCTGTGCTTCAGTGACAGAACCTTTGAACAAGTA	2963
OY	2716	GGGGAGAAAGCCATGCCACTGTTTGAAGAGTCTACTGAAAAACATCATTTGC---AGAA	2772
Db	2964	GAAAGTGAAGCCGCACTGTTAACTGAGAGGTATTGGAAAGAAATTAATTTGAGAAAGAA	3023
OY	2773	GAAACTCTGTGCTCAACCCAGACGTTACCAAGAGGTAAAGATGCCATGACAGATGTC	2832
Db	3024	GAAACCCCAACGGTTTACTGACCTCTGCCAGAGAACAGAGAGGCCCCGGGGCCACACGGTC	3083
OY	2833	ACCAAGTGAAGTGAATTCACCTTCAGAGCTGTGACAGCCACAGAGACCTTCAGAGGCTCTC	2892
Db	3084	GTTAGTGAAGCGGAATTTGACCCCGAAGCTGTGACAGCTCAGAAACTCGAGGGCCATTGG	3143
OY	2893	CGTACTGAAGAAATTCACCAAGCATGTGGGGGCCGGAAGAGACCACAGATGTGTCCGCA	2952
Db	3144	GGTTCGGAAGAGAAACCGAAGCATGTGTGTGAAGAGCCACAGAAATGTGTGACGA	3203
OY	2953	GTTTTCCACCTGACTACTGCCAGACACACAGAGAAACCCACCGATTCAGAGAGTA	3012
Db	3204	GTCTCCCAATTAACGCATCTCCAGACACCACAGAGAGGCCACTCGGTGCGAGAGAGTG	3263
OY	3013	GAGAGTGTGTGCTAGATACAGAGAAGAGAGAGCCGACAGAGCCATCTTCCAAACC	3072
Db	3264	GAAAGTGGGCTACTCAGATAGAAAGAGAAAGAGAGGGGAGCTCAAGAGTCTTCCAGGCA	3323
OY	3073	GTTTGCAGCAAGSTGAAAGAGAGTCCCAAGTCCCTGCAAC---CAGACTGTGCGAGAGA	3129
Db	3324	GTGGCGAAAAAAGTGAAGAGAGATCCCAAGCTCCGTGGCCGCGTGGCCAGAAAGATGG	3383
OY	3130	ACGGGGTCAAAAAGCACTGGAGGAAGTTGAGAGAGTGAAGAGACTCCGAAGGCTGGCT	3189
Db	3384	CTTTCAGCCTGTGCAAGAGACAGAGCAGAGCAAGAACACAGAGAGAGGCTGAGAGCTGGGT	3443
OY	3190	TCGAGAAAGAGAGACGTTATGCCAAAAGAGACCCGTGCGAGAGTGAAGTGAAGCAT	3249
Db	3444	CTGAAAGAAAGACGSGATGTAGTGTGAAGATGATGTCTCAGAGAGCAAAAACGTGAGCCT	3503
OY	3250	CTTTGACAGGGCTCTGAGACTGAGACAGGCTACTTCCAGAGAGCCTTG---AAGTTCTGAA	3306
Db	3504	TTTATACAGAGGAAGGTGGTGGGGCAGAGACCCCGAGAAAGCTTTGAAAAGGCTCTCAA	3563
OY	3307	GTACAGGCAAGATTA-----GACCATGTGGCCACGTGCCA-----	3341
Db	3564	GTTCAGAGAGACTTAAGTTCAGTGAAGCTGTTAACCATTTGTCAAGCCGAACCTTAAGCT	3623
OY	3342	--GGTATACAGGCTCAGCAGCTAGTGAACAGAGCCGTGGCCCTGTGATATCCGAAGAC	3399
Db	3624	GGGGTAAAAATCACAGAGATGGTGTGATGGAACAGGCTATCCCCCTGACTGGGTGGAAGCC	3663
OY	3400	TTTACAGACAGTGAAGCAATGGAAGCACCTCCTTAGCAGATTCAGACACTGCAAGATGG	3459

Db	4755	GTCAAGTGAAGTGAACAATTG--AGGATTTTAGACCTCGAAAATGGGATTTTGGAACTT	4811
Oy	4498	GAGAGTAAAGACAACAAGATTGTGTCGAAACGTCATTTACAGACAGCCGTTGACCAGTTTGGCA	4557
Db	4812	GAGACCAAAAAAGTAGTAACCTGTCTCAAAAACATCATCATCCAGACCGCGTTGACCAGTTTGTAA	4871
Oy	4558	CGTAC---AGAAAACAGCCCCCGAAACTCATGCTATTGATTCACAGACCAGTTTCTCTGCA	4614
Db	4872	CGTACAGACAAAACAGCAGCCAGAAATGTTGACGCTGAGAGTTACAGACACAAACCTTACGCTG	4931
Oy	4615	TGCAGGCTTGACAGACAGGGA	4634
Db	4932	ATTAAGCTGACACCCAGGA	4951

```

US-08-232-463-14/C
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOXLPOX VIRUS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 diagonal Road, Suite 500
City: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300. 6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: PTZ9pt-F1s
US-08-232-463-14

Query Match          1.9%; Score 99.8; DB 1; Length 7218;
Best Local Similarity 2.1%; Pred. No. 4,7e-15;
Matches      8; Conservative 262; Mismatches 109; Indels    0; Gaps

QY   912 AAAAGGATGATCTGGAAACTGCCGAGAGAAGAAAGAGCAAGCGACGAAGAAAAGTACA 971
      :::::::::::::::::::: : :::::::::::::::::::: : :::::::::::::::::::: :
Db    1431 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1372
QY   972 CGAGGAAGAAAAAGCAAGACAGAGCCAGCTTCGAGAGAGCAGAGAGCCGCGAAGAACAC 1031

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[illegible]

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RESULT 5
US-09-249-585A-4/c
: Sequence 4, Application US/09249585A
: Patent No. 6417002
: GENERAL INFORMATION:
: APPLICANT: Horlick, Robert
: TITLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISOMES
: FILE REFERENCE: 0867/0D905
: CURRENT APPLICATION NUMBER: US/09/249,585A
: CURRENT FILING DATE: 1999-02-11
: NUMBER OF SEQ ID NOS: 18
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO: 4
: LENGTH: 1926
: TYPE: DNA
: ORGANISM: Epstein Barr Virus
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)..(1926)
: OTHER INFORMATION: template strand of EBNA-1 DNA
US-09-249-585A-4

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Query Match	1.4%	Score 71.2	DB 4	Length 1926
Best Local Similarity	47.7%	Pred. No. 3.8e-08		
Matches 208	Conservative	0	Mismatches 228	Indels 0
			Gaps	0
QY 948	GGAGCAAGAGGCGACAGAAAAGTATGACGAGGAGAAAAGACAGACCAGCTCCGA	1007		
Db 977	GGAGGACGAGGAGCGGGGAGACGAGACGGGGAGGACGAGACGGGGAGCGGGA	918		
QY 1008	GGAGCAGGAGCCGGCGAGAAACACAGACCAGGCCAGTTGTCAGCAGACTACGAAAGT	1067		
Db 917	GGAGCAGGACCGGGCGAGGACGGGAGACGAGACCAGCGGGGAGGACGAGCAGACG	858		
QY 1068	GGAGGTGCTTTGGAGAGCCAGGTTGGTGTACTGAGCATCTGTAGAGGAAATGTTC	1127		
Db 857	GGAGGACGGGGAGGAGGACGAGGAGCGGGAGGACGGGAGGAGCAGGAGCGGGAGGA	798		
QY 1128	TCTTTGGCAACGGAGAGTGTATGAGAAAGATGGAACCCACCAAGAGTGTTCAGA	1187		
Db 797	CGGGAGGACGAGGACGGGGAGACGGGGAGACGACGAGCAGCGGGAGGACGGGAGGACA	738		
QY 1188	GGTCCACGTGAGCACCGTGGAGAAAGACAGAGGAGGAGGAGGAGGAGGAGGAGCTGA	1247		
Db 737	GGAGCGGGAGGACGAGGACGGGGAGGACGAGGACGGGGAGGACGAGGAGGAGGAGCGG	678		
QY 1248	AGGGGCGCTGCTGGTAGAAGGAGACAGGAGAACTCTTGGCCCCCTGAGAAACTBTGAGCC	1307		
Db 677	GGAGGACGGGAGGAGGAGCAGAGCAGGGGAGGAGCAGGAGCGGGAGGAGCGGAGGAGCGG	618		

OY 1308 CCAGAGAGTCCCCAGGAACTGATAGCGCTGCTGAGAGCGCTGATGAGAGACAGACAGATGTG 1367  
 Db 617 GGAGGACGAGGACGGGGAGAGACGACGAGACGGGGAGAGCGGGGAGGACGGGGAGGAGCA 558  
 OY 1368 TGTCTCTGGAGGAGAC 1383  
 Db 557 CGAGGACGGGGAGGAC 542

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RESULT 6
US-09-130-114-2/C
; Sequence 2, Application US/09130114
; Patent No. 5976807
; GENERAL INFORMATION:
; APPLICANT: Horlick, Robert A.
; APPLICANT: Damaji, Bassam B.
; APPLICANT: Robbins, Alan K.
; TITLE OF INVENTION: Eukaryotic Cells Stably Expressing Genes
; TITLE OF INVENTION: From Multiple Transfected Episomes
; FILE REFERENCE: 0867/ID903051
; CURRENT APPLICATION NUMBER: US/09/130,114
; CURRENT FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: EBNA
US-09-130-114-2

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Query Match	1.48;	Score 71.2;	DB 2;	Length 1931;
Best Local Similarity	47.78;	Pred. No. 3.8e-08;		
Matches 208; Conservative	0;	Mismatches 228;	Indels 0;	Gaps 0;

QY	948	GGGCAACAGCCACAAAAAATATAGCCGAGGAAAGAAAAGAAAAGACACAGACCCAGCCTCGGA	1007
Db	977	GGAGACACAGGACCGGGAGGACGAGGACGGGGAGGAGACAGAGACGGGGAGGACGGGGA	918
QY	1008	GGAGCAGGAGCCGGCGAGAGACACAGACCAGGCCAGGTTGTCTAGCAGACTACGAGAAGGT	1067
Db	917	GGACGAGGACCGGGAGGACGGGGGAGGACGAGACCGGGGAGAACCGGGGAGGACGAGGACGG	858
QY	1068	GGAGCTGCCTTTGGAAACCAAGTTGGTATACCTGGAGGCATGCTCAGAGCAAAAGTTGTC	1127
Db	857	GGAGACCGGGGAGGAGGACGAGGACGGGGGAGGACGGGGGAGGAGGACGAGGACGGGGAGGA	798
QY	1128	TCCTTTGGCAACGCAAAAGTTGTTTGTATGAGAGATGAGAAAGCCACACAGAAGTTGTTGAGA	1187
Db	797	CGGGAGGACCAAGGACCGGGGAGGACGGGGGAGGACAGAGAACGGGGAGGACGGGGAGGACGA	738
QY	1188	GGTCCACGTGAGCACCGTGGAGAAAGACAGAGGAGGACGACGAGGAGGAGGAGGAGAGGCTGA	1247
Db	737	GGACCGGGGAGGACGAGGACGGGGGAGGACGGGGGAGGACGAGGACGGGGGAGGACGGG	678
QY	1248	AGGGGGCGTGGTGTAGAGGAAGAACGAGAGAACTTGGCCCTGAGAAACTGGCTGAGGC	1307
Db	677	GGAGGACCGGGAGGAGGACGAGGACCGGGGAGGACGAGGACGGGGGAGGACGGGGAGGACGG	618
QY	1308	CCAGAGAGTCCCCAGGAAAGCTGAGCCTGCTGAGAGGAGCTGATGAAGACGAGAGAGATGTG	1367
Db	617	GGAGGACGAGGACGGGGAGGAGGACGAGGACCGGGGAGGACCGGGGAGGACGGGGAGGAGGA	558
QY	1368	TGTCTCTGAGAGGAGAC	1383
Db	557	CGAGGACGGGGAGGAC	542

RESULT 7  
US-09-249-585A-2  
; Sequence 2, Application US/09249585A  
; Patent No. 6417002  
; GENERAL INFORMATION:

```

? APPLICANT: Horlick, Robert
? TITLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISOMES
? FILE REFERENCE: 0867/OD905
? CURRENT APPLICATION NUMBER: US/09/249,585A
? CURRENT FILING DATE: 1999-02-11
? NUMBER OF SEQ ID NOS: 18
? SOFTWARE: Patentin version 3.0
? SEQ ID NO 2
? LENGTH: 1926
? TYPE: DNA
? ORGANISM: Epstein Barr Virus
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (1)..(1926)
? OTHER INFORMATION: coding strand of EBNA-1 DNA
US-09-249-585A-2

```

Query Match	1.4%	Score 70.8;	DB 4;	length 1926;
Best Local Similarity	45.3%;	Pred. No. 4.8e-08;		
Matches 335;	Conservative 0;	Mismatches 402;	Indels 3;	Gaps 2

QY	1914	AAAGGATGATCTGGAACACTGCCGAGAAAGGAAAGGACGACAGGACGAGAAAAGTATGACG	973
Db	333	AGGAGAGGGGACAGAGGGGACAGAGGGGACAGAGGGGACAGAGGACAGAGGAGGGGACG	392
QY	974	AGGAAGAAAAAGAAAACACAGAGCCACCTCCGAGGAGCAGAGAGCCGCGCAGAAACACAG	1033
Db	393	AGCAGAGAGAGCGGACAGAGGGGACAGAGGGGACAGAGGGGACAGAGGGGACAGAGGG	452
QY	1034	ACCAAGGCCAGTTTCTACACGACTACGAGAGGTGAGCTGCCCTTTGGAAACCCAGGTTG	1093
Db	453	AGGAGGGGACAGAGGGGACAGAGACAGAGAGGAGGGGACAGAGGGGACAGAGGGGAC	512
QY	1094	GTGACCTTGAGGACATCGMCAGAGAGAAAGTGTCTCTTGGCAACGGAAGTGTGATG	1155
Db	513	AGGAGAGGGGACAGAGACAGAGAGGAGGGGACAGAGGGGACAGAGGGGACAGAGGGGAC	572
QY	1154	AGAAATGGAAGCCACCACCAAGAAATTGTTTCAAGAGTCCACGTGAGACCCGTGAGAA	1213
Db	573	AGGGGACAGAGGGGACAGAGACAGAGAGGAGGGGACAGAGGGGACAGAGGGGACAG	632
QY	1214	CAGAGGAGGACACAGGAGAGGAGAGAGGCTTAAGGGGCGTGGTGTGAAGAACACAG	1273
Db	633	AGGGGACAGAGCA--GAGAGGGGACAGAACAGAGAGGAGGGGACAGAGGGGACAGAGGGGAC	691
QY	1274	GAGAACTCTTCCCCCTGAGAAACTGGCTGAGGCCAGGAGGGTCCCCCGAAGAGCTGAG	1333
Db	692	GAGCA--GGAAGGGCAGGAGCAGAGGGGACAGAGCAAGAGGGGACAGAGGGCAGAGGGG	749
QY	1334	CTGCTGAGGAGCTTATGATAGAGCAGAGAGATGTTGTCTCTTGAGAGGAGCCACTCTAAC	1393
Db	750	AGGAGGGGACAGACAGAGAGGGGACAGAGGGGACAGAGGGGACAGAGGGGACAGAGGGGAC	809
QY	1394	TGACAGACTTAAGTCTGGAAGAGACGCTGCCCAACACCCAGAGGCAATTGTCACTG	1453
Db	810	AGCAGAGGAGGGGACAGAGGGGACAGAGCAGAGAGGAGGAGGAGGGGACAGAGGGGAC	869
QY	1454	AGGTGAAATCTCTCTCTCAGGAAGATCAAGGTACAGGAAGTCCCTTGAAGAAAC	1513
Db	870	AGGGGACAGAGGGGACAGAGCAGAGAGGGGACAGAGGGGACAGAGGGGACAGAGGGGAC	929
QY	1514	TCTTCAGTAGCTCAAGGCTTAAAGAGCTGTCTGGGAAGAGCAGAGGGGAACACAGAG	1573
Db	930	GGCAGAGCAGGAGAGGAGGGGACAGAGGACAGAGGGGACAGAGGACAGAGGAGGAGGGG	989
QY	1574	GTGGGAGAGCAGAGAGCTTGGAATATCCACATTCACACCCGATCCAGAGAGTG	1633
Db	990	TGAGAGAGGACGTGGAGGCGGGGTTCAGAGGATTAATGGAGGCGGGGCTCGAGAGGTAG	1049
QY	1634	CTGATGAGCAGAGGAGAG	1653
Db	1050	TGGAAGCCCGCGGGGTAG	1069









```

OY 1034 ACCGGCCAGAGTTGTCACGAGTATCAGAAAGTGAGCTGCTTTGGCAAGCCAGGTTG 1093
Db 882 AGGAGGGGCGAGGAGGGGCGAGGACGACGAGAGGGGCGAGAGGGGCGAGGAGGCG 941
OY 1094 GTGACCTGGAGGAGCATGCTCGAGAGGAAAGTGTGCTCTTTGGCAAGGAGTGTGATG 1153
Db 942 AGGAGGAGGGGGCGAGAGGACAGGAGAGGGGCGAGAGGGGCGAGAGGAGGGGCGAGG 1001
OY 1154 AGAAGATGGAAGCCCAACCAAGAAATTGTTGCGAGAGTCCACGTGAGCACCGTGAGAA 1213
Db 1002 AGGGGGCGAGGGGGCGAGGACGAGGAGGAGGGGCGAGGAGCGAGAGGGGCGAGGAGG 1061
OY 1214 CAGAGGAGGAGCGAGGAGGAGGAGGAGGCTGGAAGGGGGCGGTGGTGGTGAAGGAAG 1273
Db 1062 AGGGGCGAGGAGCA-GGAGGGGCGAGGACAGGAGAGGGGCGAGGAGGGGCGAGAGGG 1120
OY 1274 GAGAAATCTTGTCCCGCCGAGAAACCTGGCTGAGCCCGAGGAGGTCCCGCAGGAAGCTGAGC 1333
Db 1121 GAGCA--CGAGGGGCGAGGACGAGGAGGGGCGAGGAGCGAGGAGGGGCGAGGAGGGGCG 1178
OY 1334 CTGCTGAGGAGCTGTATGAAAGCAGAGAGATGTGTCTCTTGAGAGAGCACACTCAAC 1393
Db 1179 AGGAGGGGCGAGGAGACAGAGGGGCGAGGAGGGGCGAGGAGGAGGAGGAGGAGGAGG 1238
OY 1394 TGACAGACCTTAATGCTTCGAAGAGAAAGCCTGCCCAACACCCAGAAAGGCAATGTGATG 1455
Db 1239 AGCGAGGAGGAGGGGCGAGGAGGGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1298
OY 1454 AGGTGAGAGATGCTCTCTCTCGAGGAAAGATCAAGGTACAGGAGGAATGCTCTGAGAGAAC 1513
Db 1299 AGGGGCGAGGAGGGGCGAGGACAGGAGGGGCGAGGAGGGGCGAGGAGGAGGAGGAGG 1358
OY 1514 TCTTCACTAGCTCAGCGCTTAAGAGAGCTGTCTGGGAAGAGCAGAAAGGGGAAACGAGAG 1573
Db 1359 GCGAGGAGAGCAGAGAGGAGGGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1418
OY 1574 GTGGGGGAGAGCAGAGACCTCTGAGAAATACCAACACTTCACACCCGAAATCCCAAGAGCTG 1633
Db 1419 TCGGAGGAGCGAGTGAGAGCCGGGGCTCGAGAGGAGTGAAGGCGGGGCTGAGAGAGTAG 1478
OY 1634 CTGATGAGCAGAGAGGAGAG 1653
Db 1479 TGGAGCGCGCGGGGTAGAG 1498

RESULT 13
US-07-884-811-15
: Sequence 15, Application US/07884811
: Patent No. 5316921
: GENERAL INFORMATION:
: APPLICANT: Godowsky1, Paul J. Lokker, Nathalie A. Mark, Melanie R.
: TITLE OF INVENTION: SINGLE-CHAIN HEPATOCYTE GROWTH FACTOR VARIANTS
: NUMBER OF SEQUENCES: 21
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 460 Point San Bruno Blvd
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: patin (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/884,811
: FILING DATE: 19920518
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:

```

Query Match	1.48;	Score 70.8;	DB 1:	Length 10596;
Best Local Similarity	45.3%;	Pred. No. 1.1e-07;		
Matches 335;	Conservative 0;	Mismatches 402;	Indels 3;	Gaps 2;
NAME: Dreger, Ginger R. REGISTRATION NUMBER: 33,055 REFERENCE/DOCKET NUMBER: 755.1 TELECOMMUNICATION INFORMATION: TELEPHONE: 415/225-3216 TELEFAX: 415/952-9881 TELEX: 910/371-7168 INFORMATION FOR SEQ ID NO: 15: SEQUENCE CHARACTERISTICS: LENGTH: 10596 bases TYPE: NUCLEIC ACID STRANDEDNESS: single TOPOLOGY: linear US-07-884-811-15				
QY 914	AAGAGATGATCTCGAAACTGCCCGAAGACAGAAAGGACCAAGGCGCAAGAAAAGTAAACG	973		
DB 2296	AGGAGAGGGGCGAGGAGGGGCGAGAGGGGCGACGAGAGGGCGAGGAGCGAGGAGGGGCGAG	2355		
QY 974	AGGAAGAAAGGAAAGACAGACAGCCAGCCCTCGAGAGACAGAGAGCCGCGCAGAAACACAG	1033		
DB 2356	AGCAGAGAGGAGGGCGAGGAGGGGCGAGAGGGGCGAGAGGGGCGAGAGAGGAGGAGGCGCAGAG	2415		
QY 1034	ACCAGGCCAGCTTGTCCAGCAGACTACGAGAAAGTGGAGCTGCTTTGGAAACCAAGTTTG	1093		
DB 2416	AGGAGGGGCGAGAGGGGCGAGAGGAGGAGGAGGGGCGAGAGGGGCGAGAGGGGCGAGAGC	2475		
QY 1094	GTGACCTGGAGGCATCTCTCAGAGGAGCAAGTGTGCTTTGGCAACGGAAGTGTGGATG	1153		
DB 2476	AGGAGAGGGGCGAGAGGAGGAGGGGCGAGAGGGGCGAGAGGGGCGAGAGGAGGGGCGAG	2535		
QY 1154	AGAAATGGAACCCACCACCAAGTTGTTGCAGAGGTCACGCTGACACCTGTGAGAGA	1213		
DB 2536	AGGGGCGAGGAGGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2595		
QY 1214	CAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1273		
DB 2596	AGGGGCGAGGAGCA - GGAGGGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2654		
QY 1274	GAGAACTCTTGGCCCTTGAGAAATCTGCTGACAGCCCGAGAGAGTCCCGCCAGAACTGACG	1333		
DB 2656	GAGCA - GGAGGGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2712		
QY 1334	CTGTGAGAGAGCTGATGAAGAGCAGAGAGATGTGTCTCTGAGAGAGCCACTCAAC	1393		
DB 2713	AGGAGAGGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2772		
QY 1394	TGACAGACCTTAAGTCCCTGAAGAAACGCTGCCCAACACCCAGAAAGGCATTGTCACTG	1453		
DB 2773	AGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2832		
QY 1454	AGGTGAGATGCTGTCTCTCAGGAAAGATCAAGGTACAAGGAGAGTCCCTTGAAGAAAC	1513		
DB 2833	AGGGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2892		
QY 1514	TCTTCAGTACGTCAGGCTTAAAGAAAGCTTCTGGGAAGAGGAGGAGGAGGAGGAGGAGGAG	1573		
DB 2893	GGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2952		
QY 1574	GTGGGGAGACAAACAGCCTTGAGAAATACCAACACTTACACCGAATCCCGAGAGAGTG	1633		
DB 2953	TGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	3012		
QY 1634	CTGATGAGCAGAAAGGAGAG 1653			
DB 3013	TGGAGGCGCCGCGGTAGAG 3032			

```
US-07-885-971-15
; Sequence 15, Application US/07885971
; Patent No. 5328837
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J., Lokker, Nathalie A., Mark, Melanie R.,
; TITLE OF INVENTION: HEPATOCYTE GROWTH FACTOR PROTEASE DOMAIN VARIANTS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/885,971
; FILING DATE: 19920518
; CLASSIFICATION: 530
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: 779
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-3216
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10596 bases
; TYPE: NUCLEIC ACID
; STRANDEDNESS: Single
; TOPOLOGY: linear
US-07-885-971-15

Query Match 1.4%; Score 70.8; DB 1; Length 10596;
Best Local Similarity 45.3%; Pred. NO. 1.1e-07;
Matches 335; Conservative 0; Mismatches 402; Indels 3; Gaps 2;

QY 914 AGAGGATATCTGGAAATGCCCGAGAGAAAGAGCAAGCAAGCAAAAAGTAGAGC 973
DB 2296 AGGAGGAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2355
QY 974 AGGAGAGAAAGAGAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1033
DB 2356 AGCAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2415
QY 1034 ACCAGGCCAGGTTGTTCAGCAGACTACGAGAAGGTGAGCTGCTTTGGAAGCAGGTTG 1093
DB 2416 AGGAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2475
QY 1094 GTGACCTGAGGATCGTAGAGAGAGAACTGTGCTCTTTGGCAACGGAAGTTTGATG 1153
DB 2476 AGGAGAGAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2535
QY 1154 AGAAGATGAGACCCCAACCAAGAGTTGTTCAGAGAGTCCAGTGAACACGAGGAGAA 1213
DB 2536 AGGGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2595
QY 1214 CAGAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1273
DB 2596 AGGGGAGAGAGCA-GGAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2654
QY 1274 GAGAACTCTTGGCCCTTGGAAGAACTGCTGAGCCCAAGAGAGTCCCAAGGAAGCTGAGC 1333
DB 2655 GAGCA--GGAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2712
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QY 1334 CTGCTGAGGAGCTGATGAAGACAGAGATGTGTCTCTGGAGAGAGCACTCAAC 1393
DB 2713 AGGAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2772
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RESULT 15
US-08-087-783A-15
; Sequence 15, Application US/08087783A
; Patent No. 5547856
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J., Lokker, Nathalie A., Mark, Melanie R.,
; TITLE OF INVENTION: HEPATOCYTE GROWTH FACTOR VARIANTS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/087,783A
; FILING DATE: 13-Jul-1993
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 07/884811
; FILING DATE: 18-May-92
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/885971
; FILING DATE: 18-May-92
; ATTORNEY/AGENT INFORMATION:
; NAME: Maisch, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P0755779P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5416
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10596 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: linear
US-08-087-783A-15

Query Match 1.4%; Score 70.8; DB 1; Length 10596;
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Best Local Similarity 45.3%; Pred. No. 1.1e-07;  
Matches 335; Conservative 0; Mismatches 402; Indels 3; Gaps 2;

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OY 974 AGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1033
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OY 1034 ACCAGGCCAGGTGTCAGCAGACTACGAGAGGTGAGCTGCCCTTTGAAAGACGAGTTG 1093
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OY 1154 AGAAGATGGAAGGCCACCAAGAGTTGTTGACAGAGTCCACGTGAGCACCCTGAGAGA 1213
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Db 2655 GAGCA--GGAGGGGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2712
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OY 1334 CTGCTGAGGAGCTGATGAGAGCAGAGAGATGTGTCTCTGAGAGAGACCACTCAAC 1393
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Db 2713 AGGAGGGGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2772
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Db 2773 AGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2832
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OY 1454 AGGTGAGATGCTGTCTCTCAAGAAAGATCAAGGTACAGGGAAGTCCCTTGAGAAAC 1513
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Search completed: December 9, 2002, 21:27:54  
Job time : 297 secs



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Qy	301	GACCGATTAAGAAATGGCGGCCAACTCACAGTGTTTGAAGATATTCACAAAGATGG	360
Db	333	GACCGATTTAAAGAAATGGCGGCCAACTCACAGTGTTTGAAGATATTCACAAAGATGG	392
Qy	361	CAGGAGAGACATCAGAAATTAATTGAACAGATCCCTGCTTCAGAAAACAATGTGAAGAA	420
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Db	453	ATGTACAGCCTGCTGAGTCCACAGGCTTAATGATGTGTGCTTCAAGAAATTTAAATT	512
Qy	481	GTGTGTTTAAATTCACGCTGAAGAAAGATTAATAATGAAGATCAGATCTGTCCAATA	540
Db	513	GTGTGTTTAAATTCACGCTGAAGAAAGATTAATAATGAAGATCAGATCTGTCCAATA	572
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Db	573	CTCACTGTCAAGAAAGATGAAGGCGAAGGGGCGAAGGCGTGTGCGAGCTGGAGACAC	632
Qy	601	CAGAGGCCAGTGTGAGACTGCCCTTCGAGAGATCAGATCCCAAGAAATGAGCTGAAG	660
Db	633	CAGAGGCCAGTGTGAGACTGCCCTTCGAGAGATCAGATCCCAAGAAATGAGCTGAAG	692
Qy	661	CAATTCACAGAGAAACAAGAGCCACCTTGAACCAAGAACAGACACACAGAAATCCC	720
Db	693	CAATTCACAGAGAAACAAGAGAGCCACCTTGAACCAAGAACAGACACAGAAATCCC	752
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Db	753	CTTCAAGCCGAATGTGATCAAGCGGCTGAGGAAAGAACCCAAAGATGAAGGAGAAAGAAA	812
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Db	873	ACATCTTCTTCAAGAAGTCTTCACTCACAGTGTGGGCGGCTGGCGCAAGAACCCAGC	932
Qy	901	TTCAAGAAATCAAAAAGAGATGTATCTGGAACCTGCCGACAAAGAAAGAGACAAGGCA	960
Db	933	TTCAAGAAATCAAAAAGAGATGTATCTGGAACCTGCCGACAAAGAAAGAGACAAGGCA	992
Qy	961	GAAGAAAGTAGACGAGGAAGAAAGAGAAAGACAGAGCCAGCCTCGAGAGAGCAGAGCCG	1020
Db	993	GAAGAAAGTAGACGAGGAAGAAAGAGAAAGACAGAGCCAGCCTCGAGAGAGCAGAGCCG	1052
Qy	1021	GCAGAGACACACAGCCAGGCGGTGTACAGACACTACAGAAAGTGTAGCTGCTTTG	1080
Db	1053	GCAGAGACACACAGCCAGGCGGTGTACAGACACTACAGAAAGTGTAGCTGCTTTG	1112
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Qy	4921	AACGGACCAAAAGCTAACCCAGAGAGGCCGATCCCCCAAAAGTTGAGGTCACAGAAAGAA	4980
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Db	5013	ATGCTCTACCAAGTCAGTCAAGAGAAACAAGGCCACAGCAGAGAGAGCACTGCAGAGCCA	5072
Qy	5041	AAGGAGACCTGGGCAAGATCTTAAGATGTTAGTTGCTCATTTGTACATCTGTAAGACAGA	5100
Db	5073	AAGGAGACCTGGGCAAGATCTTAAGATGTTAGTTGCTCATTTGTACATCTGTAAGACAGA	5132
Qy	5101	ATGGAAGAAACAATCAGACAGAAACAAGATGCTGTTGGGACCTTGACAGCAAAATTTACAG	5160
Db	5133	ATGGAAGAAACAATCAGACAGAAACAAGATGCTGTTGGGACCTTGACAGCAAAATTTACAG	5192
Qy	5161	AGCCCATGAGATCCAGAGACAGAGGCCGTTCCAAATGATTTCC	5200
Db	5193	AGCCCATGAGATCCAGAGACAGAGGCCGTTCCAAATGATTTCC	5232

RESULT 2  
US-09-902-432-1  
; Sequence 1, Application US/09902432  
; Patent No. US20020160002A1

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1  APPLICANT: Irwin H Gelman
2  APPLICANT: Susan G. Jaken
3  TITLE OF INVENTION: TUMOR SUPPRESSOR GENE
4  FILE REFERENCE: A30558-A-FWC-A 070156.0597
5  CURRENT APPLICATION NUMBER: US/09/302.432
6  CURRENT FILING DATE: 2002-04-08
7  PRIOR APPLICATION NUMBER: 08/978,277
8  PRIOR FILING DATE: 1997-11-25
9  PRIOR APPLICATION NUMBER: 08/665,401
10 PRIOR FILING DATE: 1996-06-18
11 PRIOR APPLICATION NUMBER: 08/635,121
12 PRIOR FILING DATE: 1996-04-19
13 NUMBER OF SEQ ID NOS: 35
14 SOFTWARE: FaSTSeq for Windows 4.0
15 SEQ ID NO: 1
16 LENGTH: 5134
17 TYPE: DNA
18 ORGANISM: Rattus norvegicus
19 US-09-902-432-1

```

Query Match	75.1%;	Score 3903.4;	DB 9;	Length 5134;
Best Local Similarity	97.5%;	Pred. No. 0;		
Matches 4120;	Conservative	0;	Mismatches 76;	Indels 31;
				Gaps 14;

QY	984	GGAAAGACAGAGCCACCCTTCGAGAGACGACGAGCCGGCAGAAACACAGACAGCCAG	1043
Db	1	GGAAAGACAGAGCCACCCTTCGAGAGAGCAGGACCCGGAGAAACACAGACAGCCAG	60
QY	1044	GTTGTACACACATCAGCAGAAAGGTGAGAGCTTCCTTTGAAAGACACAGTGTGGTACCTGGA	11030
Db	61	GTTGTACACACACTACAGAAAGGTGAGAGCTTCCTTTGAAAGACACAGTGTGGTACCTGGA	120
QY	1104	GGCATCGTCAGAGGAGAAAGTGTGCTCTTTGGCAACGGAAGTGTGGATGAGAGATGGA	1153
Db	121	GGCATCGTCAGAGGAGAAAGTGTGCTCTTTGGCAACGGAAGTGTGGATGAGAAATATGA	180
QY	1164	AGCCCAACCAAAATTTGTCAGAGGTCACACGTGAGACCCGTGGAGAAAGACAGAGAGAGGA	12233
Db	181	AGCCCAACCAAAATTTGTCAGAGGTCACACGTGAGACCCGTGGAGAAAGACAGAGAGGA	240
QY	1224	GCAGGAGAGAGAGAGAGAGGCTGAAGGGGCGCTGTGTGTAGAAAGAACAGAGAAATCCCTT	12833
Db	241	GCAGGAGAGAGAGAGAGAGGCTGAAGGGGCGCTGTGTGTAGAAAGAACAGAGAAATCCCTT	300
QY	1284	GCCCCCTGAGAAACTGGCTGAGGCCAGAGAGTCCCCAGAGAACTGAGCCTGCTGAGGA	1343
Db	301	GCCCCCTGAGAAACTGGCTGAGGCCAGAGAGTCCCCAGAGAACTGAGCCTGCTGAGGA	360
QY	1344	GCTGATGAAAGCGAGAGATGTGTGTCTCTGAGAGAGACACTCACTCACTACAGAGACT	1403
Db	361	GCTGATGAAAGCGAGAGATGTGTGTCTCTGAGAGAGACACTCACTCACTACAGAGACT	420
QY	1404	AAGTCTTAAGAGAAAGACGCTGCCCAACACCCAGAAAGCATTTGTCAGTAGAGTGGAGAT	14633
Db	421	AAGTCTTAAGAGAAAGACGCTGCCCAACACCCAGAAAGCATTTGTCAGTAGAGTGGAGAT	480
QY	1464	GCTGTCTCTCTCAGGAAAGAAATCAAGGTACAGGGAGATCCCTTTGAAGAAATCTTCAGTAG	15233
Db	481	GCTGTCTCTCTCAGGAAAGAAATCAAGGTACAGGGAGATCCCTTTGAAGAAATCTTCAGTAG	540
QY	1524	CTCAGAGCTTAAAGAAAGCTGTCTGGGAAAGAAAGGAGAAACGAGAGGTGGGGGAGA	15833
Db	541	CTCAGAGCTTAAAGAAAGCTGTCTGGGAAAGAAAGGAGAAACGAGAGGTGGGGGAGA	600
QY	1584	CGAAGAGCTCTGGAATATCCACACATTCACACCGAATCCCCAGAGAGTCTGATGAGACA	16433
Db	601	CGAAGAGCTCTGGAATATCCACACATTCACACCGAATCCCCAGAGAGTCTGATGAGACA	660
QY	1644	GAAAGGAGAGAGCTCTGCGTGTCCCCCGAGAGACCTGAGAGAGACACGCTGTCTGAGAA	17033
Db	661	GAAAGGAGAGAGCTCTGCGTGTCCCCCGAGAGACCTGAGAGAGACACGCTGTCTGAGAA	720
QY	1704	AGGGCCGCTGGAAGCACCCCAAGATGGGGAGCTGAGAGAAAGATCTTCCGATGAGGA	17633
Db	721	AGGGCCGCTGGAAGCA--CCCAAGATGGGGAGCTGAGAGAAAGATCTTCT--GTGGA	775
QY	1764	GAAAGAGAGAAAGGATTCATCCCTCGGGGATCCCTCAAAAAGATGGGTACACCCCAAGA	18233
Db	776	GAAAGAGAGAAAGGATTCATCCCTCGGGGATCCCTCAAAAAGATGGGTACACCCCAAGA	835
QY	1824	ACGGGTCGGAAGACCTTCTGAGATGACAAAGAGAGAGAGTCTGAGAGAGTCAAGAGCGC	18833
Db	836	AC--GGTCGGAAGACCTTCTGAGATGACAAAGAGAGAGAGTCTGAGAGAGTCAAGAGCGC	894
QY	1884	CACCTTGTCTCACTAGTATGACACAGTGTGCAAAATGCAAGATGAAGTCAAAATGTTGG	19433
Db	895	CACCTTGTCTCACTAGTATGACACAGTGTGCAAAATGCAAGATGAAGTCAAAATGTTGG	954
QY	1944	TGAGGACAAAAAGCCACAGAGAACCAAAGCTAGGGTGTGATCTTCAAGTGTCTTGGGAAGC	20033
Db	955	TGAGGACAAAAAGCCACAGAGAACCAAAGCTAGGGTGTGATCTTCAAGTGTCTTGGGAAGC	10144
QY	2004	ACTGATTTGTGTGATTCATCAAGAAAGAGACAAAGAAAGGATCCTCTTCAGATGATGA	20634
Db	1015	ACTGATTTGTGTGATTCATCAAGAAAGAGACAAAGAAAGGATCCTCTTCTCA--GTAT	10711
QY	2064	AGGAGGGCCAAAGCACTGTGGGA--GGGGACAGTTCACAGACACAGAGAGGCTCACAAAGACA	21222

Db	1072	AAGAGGCCAAGGACACTGGGAGGGGAGACAGTACAGACCAAGAGGCGCCACGAAAGCA	11313
OY	2123	AAGAAGCCGGAACAGACGCTGTTCTTGCCAGCACCCAGGAGCAGGACCAAGGCGAAGAA	21822
Db	1132	AAGAAGCC - GAAAGAGCGCTGTTCGTGCACAGACCCAGGAGCAGGACCAAGCGCAAGGAA	11890
OY	2183	GTTCCCTCACCCGAGCCAGCGGGGAAAGCCCTTCGGAAGGGAAGGTGTCTCCACTTGGAGT	22422
Db	1191	GTTCCCTCACCCGAGCCAGCGGGGAAAGCCCTTCGGAAGGGAAGGTGTCTCCACTTGGAGT	12505
OY	2243	CATTAAAGATTTGTGACTCTCAAGAAAAAAATTCGAAGTCAAACTCGGAAGGAAGAACCG	23020
Db	1251	CATTAAAGATTTGTGACTCTCAAGAAAAAAATTCGAAGTCAAACTCGGAAGGAAGGAAG	13101
OY	2303	AAGACTGTAGTGTAGAG - - - - - CAGTTGTCCACTGATGATCGAACCGAGTGAAGAGA	23544
Db	1311	CCGGAAAGGACTGTGTGTAGAGAGCAAGTTGTCACTGAGATCGAACCGTGTAGAGAA	13707
OY	2335	ATCTTGGGTTTCCATTAAAGAAATTCATCCCGGAGCGCGGGAAGAAAAAGGCGAGCGGAA	24144
Db	1371	ATCTTGGGTTTCCATTAAAGAAATTCATCCCGGAGCGCGGGAAGAAAAAGGCGAGTGGAA	14300
OY	2415	- GCAAGAAACAAAGCCACTGTGTGGGAAGACTCAGAGGCGCATGGAATAAATGAGGACACCTA	24737
Db	1431	GCGAAGAACAAAGCCACTGTGTGGGAAGACTCAGAGGCGCATGGAATAAATGAGGACGACCTG	14900
OY	2474	ATGTCCAGACCGCTGTCCTCTGTCTGAGTATATCATGTGAGAGGAGGGAAGATGAGAG	25333
Db	1491	ATGTCCAGACCGCTGTCCTCTGTCTGAGTATATCATGTGAGAGGAGGGAAGATGAGAG	15500
OY	2534	CCAGGGGAATACGGAGCTGCCCCAGCTCTGTGGGGCTGTGACGTGTCGAGAGCTCA	25933
Db	1551	CCAGGGGAATACGGAGCTGCCCCAGCTCTGTGGGGCTGTGACGTGTCGAGAGCTCA	16077
OY	2554	GTAAGACTGTGTGTCCACACTGTGAGTGTGCGACATCATTTATGTGGACACAGGCGACTACCA	26533
Db	1608	GTAAGACTGTGTGTCCACACTGTGAGTGTGCGACATCATTTATGTGGAGCACAGGCGACTACCA	16677
OY	2654	GTTGTCGAAGAGCGGTGCTCTGTGTGGAATTCGCGTTCCGTAACAGACCTCTTGAACCA	27133
Db	1668	GTTGTCGAAGAGCGGTGCTCTGTGTGGAATTCGCGTTCCGTAACAGACCTCTTGAACCA	17277
OY	2714	CAGCGGAGAGAACCATATGCCACTGTTGAAGAGGTCACTAAAAAGACATCATTCGAGAG	27733
Db	1728	CAGCGGAGAGAACCATATGCCACTGTTGAAGAGGTCACTAAAAAGACATCATTCGAGAG	17877
OY	2774	AAATCTGTGTGTACCCAGACGTTACACAGAGGGTTAAGATGCCATGACGACATGTCA	28333
Db	1788	AAATCTGTGTGTACCCAGACGTTACACAGAGGGTTAAGATGCCATGACGACATGTCA	18477
OY	2834	CCACTGGAAGTGAATTTACCTTCAGAGCGTGTGACACCCACAGACACTCAGAGGCTGCC	28933
Db	1848	CCACTGGAAGTGAATTTACCTTCAGAGCGTGTGACACCCACAGACACTCAGAGGCTGCC	19077
OY	2894	GTACTGAAGAATTTACGAGACATTCGGGGGCGGAAGAGACCAACACATGTGTCCGAG	29533
Db	1908	GTACTGAAGAATTTACGAGACATTCGGGGGCGGAAGAGACCAACACATGTGTCCGAG	19677
OY	2954	TTTCCCGACTGACTGACTCCCGACACACACAGAGAGCCACCCGAGTTACAGAGGTAG	30133
Db	1968	TTTCCCGACTGACTGACTCCCGACACACACAGAGAGCCACCCGAGTTACAGAGGTAG	20277
OY	3014	AGATGGTGTGTAGATATACGAAGAAGAGAGAGCGCCAGAGCGAGGCCATCTCCAAAGCG	30733
Db	2028	AGATGGTGTGTGTAGATATACGAAGAAGAGAGAGCGCCAGAGCGAGGCCATCTCCAAAGCG	20877
OY	3074	TTTGACAGCAAGGTGAAGAAGAGAGTCCCAAGGTGCTCAACCCAGACTGTGCAGAGACGG	31333
Db	2088	TTTGACAGCAAGGTGAAGAAGAGAGTCCCAAGGTGCTCAACCCAGACTGTGCAGAGACGG	21477
OY	3134	GGTCAAAAGCACTTGAGAGAGTTGAGAGGTGAGAGGAGCTCCGAAATGTGCTTGCG	31933

Db	2148	GGTCAAAAGCACTGGAGAACAGTGTGAGAGGTAGAGAGACTGCCAATGCTGGCTTGGC	2207
QY	3194	AGAAAGAGAAAGAGCGTTATCCGAAAGAGACCCTGCGAGAACTGGAGCTGAGCATCTTGG	3253
Db	2208	AGAAAGAGAAAGAGCGTTATCCGAAAGAGACCCTGCGAGAACTGGAGACTGGAGCATCTTGG	2267
QY	3224	CACAGGGCTCTGAGACTGGACAGGCTTACTCAGAGAGCTTGAAGTTCCTGAAGTACAGG	3313
Db	2268	CACAGGGCTCTGAGACTGGAGAGGCTTACTCAGAGAGCTTGAAGTTCCTGAAGTACAGG	2327
QY	3314	CAGATGTAGACATGATGTCGCCAGGTGGCAGTTATCAAGTCTCAGAGAGCTGATGTGAACAGG	3373
Db	2328	CAGATGTAGACATGATGTCGCCAGGTGGCAGTTATCAAGTCTCAGAGAGCTGATGTGAACAGG	2387
QY	3374	CCGTGGCCCCCTGAGTGCATCCGAAACCTTGCAGACAGTAGACAAATGGAAGCACTCCCT	3433
Db	2388	CCGTGGCCCCCTGAGTGCATCCGAAACCTTGCAGACAGTAGACAAATGGAAGCACTCCCT	2447
QY	3434	TAGCAGATTCAAGACACTGCGATGGGACACAGCAGAGTGAACCAATTGACAGCCAGGACA	3493
Db	2448	TAGCAGATTCAAGACACTGCGATGGGACACAGCAGAGTGAACCAATTGACAGCCAGGACA	2507
QY	3494	GTAAGGCCACTGCAAGCTGTGAGGCACTCACAGTCAACAAABAAGGCGCTACTGCTC	3553
Db	2508	GTAAGGCCACTGCAAGCTGTGAGGCACTCACAGTCAACAAABAAGGCGCTACTGCTC	2567
QY	3554	AGAAAGAGAGAGCCCTGCGACACTACCTAAATAATGTTCCACCCAGAGAAACATGGGGAG	3613
Db	2568	AGAAAGAGAGAGCCCTGCGACACTACCTAAATAATGTTCCACCCAGAGAAACATGGGGAG	2627
QY	3614	AACGAGAGAGAGATGTTCTTGAACCTACACAGCAAGAGCTTACTCTGCAGCCGTGCCG	3673
Db	2628	AACGAGAGAGAGATGTTCTTGAACCTACACAGCAAGAGCTTACTCTGCAGCCGTGCCG	2687
QY	3674	TTCTGCGAAAGACTGAGGTGGTTCGAAGAGGGTGTAGTTGACTGTTGGATGGAGAAAAG	3733
Db	2688	TTCTGCGAAAGACTGAGGTGGTTCGAAGAGGGTGTAGTTGACTGTTGGATGGAGAAAAG	2747
QY	3734	TCAAGAAGAAAGACAGAGGGTGTGTAACCTGCGAACCCCAACAGTCAAAAGGCTGCTGATG	3793
Db	2748	TCAAGAAGAAAGACAGAGGGTGTGTAACCTGCGAACCCCAACAGTCAAAAGGCTGCTGATG	2807
QY	3794	TGACATATGACAGTGAAGTGTATGGAGTGGCCGGGTGTGAGAGAAAGAGAGTACTGAG	3853
Db	2808	TGACATATGACAGTGAAGTGTATGGAGTGGCCGGGTGTGAGAGAAAGAGAGTACTGAG	2867
QY	3854	TGCGAGAGTCTTACGCTTGGAGAGAGGAGAGATGGAACTGTACCTTAAGAGAGAAAAGG	3913
Db	2868	TGCGAGAGTCTTACGCTTGGAGAGAGGAGAGATGGAACTGTACCTTAAGAGAGAAAAGG	2927
QY	3914	AGCAAAAGCCAGAGCAAGTAGTAGAGAGAGGTGAGAGGAAACACCTCTCTGACATG	3973
Db	2928	AGCAAAAGCCAGAGCAAGTAGTAGAGAGAGGTGAGAGGAAACACCTCTCTGACATG	2987
QY	3974	AAGGAACCTACGGGGAAGCCAGTCTCTACACTTGGACATGCCAGCTCAGAGAGGGGGAGG	4033
Db	2988	AAAAGCACTACGGGGAAGCCAGTCTCTGACACTTGGACATGCCAGCTCAGAGAGGGGGAGG	3047
QY	4034	CACCTGGGAAGCCTTGGAGAGAGCCCTTCTCTCCAGACCAAGACAAGCGTTGCATAG	4093
Db	3048	CACCTGGGAAGCCTTGGAGAGAGCCCTTCTCTCCAGACCAAGACAAGCGTTGCATAG	3107
QY	4094	AGGTTCAAGTTCAAAAGCTGGGACACAACAGTCACTCAACACACAGAACCTGTGAAAAAG	4153
Db	3108	AGGTTCAAGTTCAAAAGCTGGGACACAACAGTCACTCAACACACAGAACCTGTGAAAAAG	3167
QY	4154	TCATAGAAAGCGTTGTGATTCAGACACAGGTGAAGTCCAGAGTGTGAGGTGCACACT	4213
Db	3168	TCATAGAAAGCGTTGTGATTCAGACACAGGTGAAGTCCAGAGTGTGAGGTGCACACT	3227
QY	4214	TATTACACGCTGAGAAAGTCTCTGCAACGGGTGGCCACTGGACTTTACAGATGCAGAG	4273
Db	3228	TATTACACGCTGAGAAAGTCTCTGCAACGGGTGGCCACTGGACTTTACAGATGCAGAG	3287



OY	667	ACGAGAAAGCAAGAAGGCCACCTCGTAAGCAAGAACAGAGACACAGAAATCCCTCTTAA	726
Db	703	ACAGAGAAACCCGAAAGACCTCGTAAGCGTGAGCAAGAACCCAGAGAAATCTCTCCCA	762
OY	727	GCCGAAATCTGATCAAGAGGCGCTGAGAGAAAGCCAAAGATGAAGAGAAAGAAACAAG	786
Db	763	GCCGAAATCTGGCCAA---GCAGTGGAGGAATGCAAGAGAGAAAGAGAAAGCAAGAA	819
OY	787	AAAGAGCCACCAAGATCCCGAGAAATCCCGAGCAGCCAGTCCACAGTGAGACACATCT	846
Db	820	AAAGACCTTGACAAAGTGTGCAGAAATCTCCGACTAGTCCCGTACCAGATGAACAGATCA	879
OY	847	TCCTTCAAGAAGTTCCTCACTCAGCGTTGGGCGCGTGGCCAGAAAGCACGTTCAAG	906
Db	880	ACCTTCAAAAATTCCTCACTCAAGGTTGGGCGCGTGGCCGCAAAAAGCACGTTTCAGG	939
OY	907	AAATCAAAAAGGATGTATCTGGAAGTGCCTGCAGCAAGAGAAAGACCAAGAGGCGACAAA	966
Db	940	AAAGCCGAAGGAGGTGAAGTGGAAAGCTTCAGAGCAAAAGAAACAAAGAGCCAGAAAA	999
OY	967	GTAGACGAGGAGAAAAGAAAGAACAGACAGCCAGCCTCGAGAG-----	1010
Db	1000	GTACACACAGAAAGAGAGCGGAAAGGACAGAGTTGCTCCGAGAAACTGACCCCTCCGAG	1059
OY	1011	-----GCAGAGCCGCGAGAAAGACACAGACAGCAGGCGTTGTCAACAGACTAC	1059
Db	1060	CAACCCACACCCACAGAGAGCCGCGCAGAAAGGCCACAGAGCCCGGTTATCACTGATAT	1119
OY	1060	GAGAAAGTGAGAGTCCCTTTGGAAGACAGAGTTGGTGGACTGAGAGCATCGTCAGAGAG	1119
Db	1120	GAGAAAGTGAAGTGGCCCTTAGAGAGAGCAAGTGAAGTGGCTCCAGAGGACTTGTGAAG	1179
OY	1120	AAGTGTCTCTCTTTGGCAACGAGAGTGTGTGATGACAAATGGAAGCCACCAAGAA---	1176
Db	1180	AAACCTGCTCGTTGGGACAGAAAGTGTGTGATGAGAAATAGAGTCCACCAAGAGAG	1239
OY	1177	GTTGTTCAAGAGTCCACGTGAGCACCGTGAGAGACAGAGGAGAGCAGGAGAGAGCA	1236
Db	1240	GTTTGGCCCGAAGTCCACGTCAACACCGTGAGAGAGAGAAACGGAAGAGAGAAAC---	1295
OY	1237	GGAAGAGCTGAAGGGGCGTGGTGAAGAAACAGAGAAATCCTTGCCCTGTAGAA	1236
Db	1296	-----GGAAGTGGAAAGAAACGAGGGTGTGTGCGACGTGAAGAA	1335
OY	1297	CTGGCTAGCCCCAGAGAGTCCCCCAAGAGAGCTGAGACCTGCTGAGAGCCTGATGAAG	1356
Db	1336	TGTTGTTGAATGATGTCAGAAAGCTCAGAAAGCCGAACCTGCCAAGAGACTGTTGAAGCT	1395
OY	1357	AGAGAGATGTGTGTTCTGTGGAGAGACCACTCAACTGACAGACTAAGTCTTGAAAG	1416
Db	1396	AAAGAAACGTGTGTTTCCGAGAGAGACCTTACACAGAGGAGTGCACCTCAGTCTTAG	1455
OY	1417	AAGAGCGTGGCCAAACCCAGAAAGCAATTTGTCAGTGAAGTGGABAATGCTGTCTCTAG	1476
Db	1456	AAGTGTGTGTCAAACCCCGAAGGCGTTGTGATGAGAGTGGAAATCTGTCAACACAG	1515
OY	1477	GAAAGAAATCAAGTACAGGGAATGCTCCCTTGAAGAAATCTTTAGTAGTCAAGCGCTTAAG	1536
Db	1516	GAGAGAAATGAAGGTGAGAGGGAATCCACTTAAAGAGCTTTTACAGCACTAGGCTTAA	1575
OY	1537	AAGCTGTCTGGGAAAGCAAGAGGGGAAACGAGAGGTGGGGGAGACGAAGAGCTTGA	1596
Db	1576	AAGCTTCTGGAAGAAACAGAAAGGAGAAAGAGCA---GAGAGAGAGAGAAATCAGG	1632
OY	1597	GAAATCCACACATTCACACCGAAATCCCCAGAGAGTGTGATGACACAGAGGAGAGAGC	1656
Db	1633	GAGACACACTAGGTTCCAGCCGATTCCTCCGACAGCCAGAGAGAACAAAGGGCGAGAGC	1692
OY	1657	TCTGCGTGTGCCCCCGAGAGAGCTGAGAGAGACAGTGTCTGGAAGAAAGGGCGGTGAA	1716
Db	1693	TCTGCTCATATCCCTTGAGAGAGCCCGAGAGAGATACGTTGTGAAAAGGGCTTAGCCAG	1752
OY	1717	GCACCCACAGATGGGGAAGCTGAAGAAAGAACTACTTCCGATGGAGAGACAGAGAGAA	1776

Db	1753	GTGCAGCAGCGATGGGGAAAGCTGGAAGAAAGGAGCTACTTCGATGAGAGAGAAAAAGAGAA	181211
QY	1777	GGGATCACTCCCTCGGATCCTTCCTCAAAAATATGGTATACACCCAAAGAAAGGGTCCGAGA	183610
Db	1813	GGTGTCACTCCCTGGGCATCTTCTAAAAAGATGGTATACGCCCAAGACGGTGTATGACGG	18727
QY	1837	CCCTTGTGAGAGTGAACAAGGAGGAGAGAGCTGGAGAGGTGACAGAGCCACCTTGTCTCC	189810
Db	1873	CCCTTGGAAAGTGAATAAAGAAAGATGAGACTGGACAGAGTCAAGAGCGCTACCTTGTCTTC	193210
QY	1897	ACTGATACACAGTGTACAAATGCAAGATGAAGTCAAAACTGTGGTGAACAACAAAG	195610
Db	1933	ACCGAGACACAGCCCTCTGAATATGCAAGAAATGAAGAGGAGCGCTGGAGAGCCAAAG	199210
QY	1957	CCAGGGAACCAAGCGGTAGGAGGAGTACTGCTGCTCTTTGGGAACACTGATTTGTCTC	201610
Db	1993	CCGGAGAACCAAAAGCCCAAGGTGATACCTCAGTATCTTGGGAACCTTAAATTTGTGTG	205210
QY	2017	GGATCATCCAAAGAGAGAGCAAGAGAGCATCTCTTCCTAGATGATGAAGAGAGCGCCAAAG	207610
Db	2053	GGATCATCCAAAGAAACAGCAGAGAGAGAGTCTCTCTTGTATGAGAGAGGGGACCMAAA	211210
QY	2077	ACACTGGAGGGGACAGTCAACAGCAGAGAGGCCACGACAAAGACAAAGACCCGGAA	213810
Db	2113	GCAATGGAGAGAGACACCAAGAAAGCTGATGAGCGCCGGAAGAAAGACAAAGAGCGGGACA	21727
QY	2137	GACCGTGTCTCGCACACCTCCACCCAGACAGACAGACAGCCAGCCAGAGAAATCTCCACCAG	219810
Db	2173	GACGGGATCTTGTGTGTCTCCCAAGAACATGATCCAGGGCGAGGAAATGCTCTCCCGGAG	223210
QY	2197	CCAGCGGGAAGCCCTTCGGAAGGGGAAAGTGTCTCCACTTGGGAGCTATTTAAAGATTA	225610
Db	2233	CAAGTGGGAACCTACCGAAAGGGAGGGGCTTCCACCTGGGAGCTATTTAAAGGTTA	229210
QY	2257	GTCACCTCCAGAAAAATCCAGTCAAACTGGAAGAGAAAGCCGGAAC-----	230710
Db	2293	GTCAAGCCCAAAAAAATCAAAAGTCCAAAGCTGGAAGAAAAAGGAGACATCCATAGCT	235210
QY	2308	---TCTNOTGTAGAGCAAGTGTGTCACTGATGTGAACCCAGTAGAGAAATCTTGGGTT	236410
Db	2353	GGGTGTGTGTAGAACATTTCCATCTCCAGACTGAAACCCGGTAAAGAAATCTTGGGTT	241210
QY	2365	TCCATTAAGAATTCATCCCGGCGGCGGCAAAAAAGGGCAGCGGAGCAACAAACAA	242410
Db	2413	TCATCAAGAGTTATTCTCGGACGAAGAAATAAAAGGCCAGATGTGGAAACAAACAA	24727
QY	2425	GCCACTGTGAAGACTCAGGGGCCAGTGAAGATAAATGAGAGCAGACCTAATGTCCAGCC	248410
Db	2473	GCCCTGTGTGAAGACGAGGAGGCCAACAGGGGCCCAAGAGATGACTGTATGTCCCGCC	253210
QY	2485	GTCCGCTCTGTGTGTGATTAATGCAAGTGAAGGAGGAGAAAGTGS-----AAACC	253510
Db	2533	GTGGTCCCTGTGTGTGATGATGATGATGATGAAGAAAGGAGAAATGAGAGCAGCAACACC	259210
QY	2536	CAGGGGAATACGAGCTGAGCCCAAGCTGCTGGGGGCTGTGTACGTGTCCGAGGAGCTCAGT	259910
Db	2593	CAAAAAAGCCGACAGACAGCCCGAGACAGAGGACAGCCACTGAGGTGTCCAAGAGCTCAGC	265210
QY	2596	AAGACTGTGTCCACTGTGAGTGTGCACTATTTGATGGGACAGGGCACTGTCCACAGT	265510
Db	2653	GAGAGTCAAGTTCAATGATGATGAGCAGCAGCTGTGCTGACGGGCGAGGGCAGCTACATTT	271210
QY	2656	GTCGAAGAGCGGTCTCTTCTGTGATATTCGCTCTCCGTAAACAGAACTTTTGAACACA	271510
Db	2713	ATTGAAGAAAGTCTCTCTTGTGATATGTCTTTCAGTACAGAAACCTTTGAAACAAAGTA	272710
QY	2716	GCGGGAAGAGCATGCAACCTGTTGAAGAGGTCACTGAAAAAGACATAATGSC---AAGAA	272210
Db	2773	GAACTGAAGCCGACTGTTAAGTGAAGAGATTTTGAAGAGAAAGTAAATTTGCAAGAA	283210
QY	2773	GAAACTCTGTGTCAACCCAGAGCTTAACAGAGAGGTGAAGAGTCCCATATGACATGTGTC	283210









Db	1884	TCCTCCTCATCCCTTGAGGAGGCCCGAGGAGATCAGCTGTCTGTGAAGAGGGCTTACGCCAG	1945
Qy	1717	GCACCCACAGATGGGGAAAGCTGAGAAAGGAACCTACTTCCGATGAGAGAAAGAGAGAA	1776
Db	1944	GTGACAGCAGGATGGGGAAGCTGAAGAAAGAGAGCTACTCCGATGAGAGAAAAAGAGAA	2003
Qy	1777	GGGATCACTCCCTGGGCATCTTCAAAAAGATGTGACACCCAGAAACGGGTCCGAGAA	1836
Db	2004	GGTGTCACTCCCTGGGCATCTTCAAAAAGATGTGACACCCAGAAACGGGTGATGACGG	2063
Qy	1837	CCCTTGTGAGGTGCAAGGAGGAAAGCTGAGAAAGGTCAACAGCGCCACTTGTCTCC	1896
Db	2064	CTTTCGGAAGTGTATTAAGAAAGATGAGCTGTGACAGAGTCAGAGGGCTACTTGTCTCC	2123
Qy	1897	ACTGATAGCACAGTGTCAAGAAATGCAAGATGAAGTCAAAACTGTTGTGAGGAACAAAG	1956
Db	2124	ACCGAGAGCACAGCTCTGTGAATATGCAAGAAATGAAGAGGAGCGTGAAGAGCCAAAG	2183
Qy	1957	CCAGAGAACCAAGAGCTAGCGTGGATACTTCACTGTCTTGGGAAGCACTGATTTGTCTC	2016
Db	2184	CCGGAAGAACCAAGGCCAAGGCGGATACCTAGATATCTTGGGAAGCTTAAATTTGTGTG	2243
Qy	2017	GGATATATCCAAAGAGAGGAGCAAGGAAGGCATCCCTTTCAGATGATGAAGGAGCGCAAG	2076
Db	2244	GGATATATCCAAAGAAAGAGGAGCAAGGAAGGCATCCCTTTCAGATGATGAAGGAGCGCAAG	2303
Qy	2077	ACACTGGAGGAGGACACTCACAGAGCAGAGAGAGGCCACGAAAGACAAAGACCGGAGCA	2136
Db	2304	GCATGGGAGGAGAGACCCACGAAAGAGTGATGAGGCGGAAAGACAAAGAGACGGGAGCA	2363
Qy	2137	GACGCTGTCTCTGCCACAGCACCAGAGACAGACACCAAGGCCAAGAAATTCCTCACCCGAG	2196
Db	2364	GACGGGATCTTGTGTGTCTCCAAAGAACATGATCCAGGGCAGAGGAATTCCTCCCGGAG	2423
Qy	2197	CCAGGAGGAGACCCCTTCCGAAGGGGAAAGCTGTCTCACCTGGGAGCTATTTAAAGATTA	2256
Db	2424	CAGGCTGGAAACCTTACCAGAGGGGAGGCGCTTTCACCTGGGAGTCTTTAAAGGTTA	2483
Qy	2257	GTCACTCCCAAAAAAATCCCAAGTCAAACTGGAAGAGAAAGCCGAAAGC-----	2307
Db	2484	GTCACTCCCAAAAAAATCCCAAGTCAAACTGGAAGAGAAAGCCGAAAGC-----	2543
Qy	2308	---TCTAGTGAAGCAAGTGTCTCACTGAGATGAAACCCAGTATGAGAGAAATCTTGGCTT	2364
Db	2544	GGGTCTGTGTGAACAATTCACATCCACAGACATCAACCCGATTAAGAAATAATCTGGGTC	2603
Qy	2365	TCCATTAAAGAAATTCATCCCGGAGCGCGGCAAAAAAAGGCGAGACGGGAACCAACAA	2424
Db	2604	TCAATCAAGAAATTTATTTCTGTGACGACAGGAABAAAAGCCAGATGTGGAACACAGACAA	2663
Qy	2425	GCACATGTGGAAGACTAGGCGCCAGTGTGAATTAATAGAGACGACCTTAATGTCCACCC	2484
Db	2664	GCCTCTGTGGAAGAGCGAGGCGCCAAACGAGGCGCAACGAAAGATGACTGTATGTCCGGCC	2723
Qy	2485	GTCTGTCTCTGTGTGAGTATATGCACTGTGAGAGGAGAGATGG-----AACCC	2535
Db	2724	GTGTCTCTCTGTGTGAGTATGATGTGTGAAGAGGAGAAATGTGAGGACACAGCAACC	2783
Qy	2536	CAGGGGAATAGGAGAGTCCCCCACTGCTGTGGGGGCTGTGACTGTGCCAGAGAGTCACT	2595
Db	2784	CAAAAAAGCGCAGCACACCCCGACCAACAABAGCACCACTGAGGTGTCCAAGAGCTCAGC	2843
Qy	2596	AAGACTGTGTGCACACTGTGATGTGCGCATGATTAATGATGGAGCACAGGCACTCAACAGT	2655
Db	2844	GAGAGTCAAGTTTCAATATGATGTGGCAGCAGCTGTGTGACGGGACAGGGCAGCTACATTT	2903
Qy	2656	GTGGAAGAGCGGTCTCTTCTGTGATATCCGCTTCGATACAGAACCTTTGAACACACA	2715
Db	2904	ATTGAAGAAAGGTCTCCTTTGTGATATGTGCTTCAAGTGCACAGAACCTCTTGAACAGTA	2963
Qy	2716	GGCGGAGAAAGCCATCCACTGTTTGAAGAGGTCACGTGAAAAAGCATCTTCC---AGAA	2772
Db	2964	GAACTGTAAAGCCGCACTTTAACTGAGAGAGTATTGGAAAAAGCACTTAATTTACAAGAA	3023

OY	2773	GAAACTCCTGTGCTCAACCCAGACGTTACCAAGAGGGTAAAGATGCCATGACAGCATGTC	2832
Db	3024	GAACCCCCCACGGTTACTGTAACCTCTGCCAGAGAAACAGAGAGGGCCGGGGGACACGGTC	3083
OY	2833	ACCAAGTAAAGGATTTTCACTCTAGAAAGCTGTGACAGCCACAGACACTCTAGAGCTCTC	2892
Db	3084	GTTAGTGGGGGAAATTGACCCCGAAGCTGTGACAGCTGCGAANAACCTGACGGSCATTG	3143
OY	2893	CGTACTGAAAGATTATACCGAAGCATGGGGGGCCGGAAGACACAGACATGGTGTCCGA	2952
Db	3144	GTTTCCGAAGAAGAACCCGAAGATCTGCTGCTGAAGAGACACAGAAATGGTGTACGA	3203
OY	2953	GTTTCCAGCTGACTGACTCCCAAGACACCAAGAGAAAGCCACCCGATTCAGAGAGTA	3012
Db	3204	GTTCCCGAGTTAAACCGACTCCCGAGACACCAAGAGAGGGCCACATCCGGTCAGAGAGTG	3263
OY	3013	GAGAGTGGTGTGCTAGTATACAGAAAGAGAGAGCGCCAGACGACAGCCATGCTCCAAAGCC	3072
Db	3264	GAAAGTGGCGTACTGTACATAGAAAGACAGAGAGAGCGGACTCAAGAGGTCTCCAGAGCA	3323
OY	3073	GTTGGAGACAGGTTGAAGAGAGAGTGCCAGGTGCCGTGCAMC--CAGACTGTGCAGAGA	3129
Db	3324	GTTGGAGAAAAAGTGAAGAGAGATCCAGAGCTCGTGGACCGGTGGGCCAGAAAGATGTG	3383
OY	3130	ACGGGGTCAAAAGCATGGAAGGTTTGAAGAGATGAGAGAGACTCCGAAGTGTGGCT	3189
Db	3384	GTTTACGCTGTGCGAGAGAGAGGAGGAGCAAGAAAGCCAGAAAGACAGCGTCAAGCTCGGGT	3443
OY	3190	TGCGAAGAAAGAGAGAGCGTTATGCGAAAGAGCCCGTGCAGAAAGCTGGAGAGTGCAGAT	3249
Db	3444	CTGAAGAAAGAGAGCGATGTGATGTTGAAAGTATGATGCTCAGAGAGGCAAAAACCTGAGCT	3503
OY	3250	CTTGGACAGAGGCTCTGAGACTGTGACAGAGGCTACTCCAGAGAGCTTGG--AAGTTCTGAA	3306
Db	3504	TTTACACAAGGAAAGGTGTGTGGGCGAACACCCAGAAAGGTTTGAAAAAGCTCTCAAA	3563
OY	3307	GTCACGGCAGATGTA-----GACCATGTCCGACGTCCA-----	3341
Db	3564	GTCACAGAGACATATGAGTGCAGTGCAGCTTGTAAACCATGTTCAGACCGAAACCTTACT	3623
OY	3342	--GTTTATCAAGCTCCAGACAGCTGATGGAACAGGCGGTGGCCCTGAGCTATCCGAAC	3329
Db	3624	GGGGTAAATACAGAGAGATGTGATGGAACAAGCATATCCCCCTGACTCGGTGTAAGC	3683
OY	3400	TTCAGACAGACTGAGACAATAATGAGACACTCCCTTAGCAGATTTCAGACACTGCATGAGG	3459
Db	3684	CCTACAGACAGTGAAGCTGATGGAAGACCCCGCTGAGCCAGCTTTGAGCCACACAGACGA	3743
OY	3460	ACACAGCAAGATGAACACATTGACGCGCAGAGAGTAAAGCCATGTCACTGCATGACGAG	3519
Db	3744	ACCCAGAAAGACGAGATTGTGGAATCTCAGAGAAATGAGGTGCATCTGTATCCAG	3803
OY	3520	TCACAGCTCACAGAAAGAGGGCGGCTACTGCTCAAGAAAGAGAGGCTTCGACACTACT	3579
Db	3804	TCAGGGGGCACAGAACCGCAGAGCGCTGTCGCAACAAAGAGGCTTCACACACTTCC	3863
OY	3580	AATTAATGTTCCAGCCACAGAGAACATGAGGGGAGAAACACAGAAAGATTTGTAAACCT	3639
Db	3864	ACTTTTGTGTTCCAGAGAAATCTAAAGAAACAATCAAGATGGAGACACTTATAGAGAT	3923
OY	3640	ACACAGCAAGAGCTTACTGCTGCAGCCGCTGCTTCTGGCAAAAGACTGAGTGGGTCAA	3699
Db	3924	AAGAGTAAAGAGGTCTCAGTGGAAATCTGTATCATCTTGTCAAAAGCTGAGGGGACTCA	3983
OY	3700	GAGGGTGA-----GGTTGACTGTGTGATGAGAAAAAGTCAAAAGACAGACAG	3750
Db	3984	GAGGCTGACACAGTATGCTGATGAGAAAAACCAAGACGTACCATTTTTCGAAGGACTTGAG	4043
OY	3751	GTGTTTGTACACTCTGG-----ACCAACAAGTCAAAAAGGCTGTGATGTGACATATGAC	3804
Db	4044	GGGTATTATAGACACAGGCTATATACGTACAGTGGGAAAGGCTCACTGCAAGTCTCCCTTAAA	4103

OY	3805	AGTAAAGTATGGGACGTGGCGGGGTGTCAGGAAAAGGAGATGACGAGTGCAGAG-----	3860
Db	4104	GGTGAAGGACAGAAAGAGCTGATATTAATAAAGATGATGCTTGAACCTGGAGAGTCAC	4163
OY	3861	-----TCTTACCCTGGAGAGGAGGAGATGGAAACTGACGTTGAAAAGGAGANA	3909
Db	4164	GCTAAGTCTCTCCATCCCGCGTAGAGAGATGCTGTTCAAGTGTGAAAAGGAGANA	4223
OY	3910	AGGGAGACAAAGCCAGAGCAAGTGAAG---AAGTGACAGAGAAAACAGCCGCTCT	3966
Db	4224	ACGAACACAGAGCCCAACCCCTGTGAATGAAAGAAACCTTGACACAGAAAACAGCTGTTCAC	4283
OY	3967	GAGCATGAAGAAACCTCAGGGAAGCCAGTCCGACACTTGAATGCTCCAGCTCAGAGAG	4026
Db	4284	GTATCTGAAGAGGTCACTAAGCAGCTCTCCAGACAGTAAATGTGCCATCTATGATGG	4333
OY	4027	GGGAGGCACTGGGAAAGCCTTGGAGGAAGCCCTTC---TCCAGACCAAGACAAAGCA	4083
Db	4344	GCAAGAGACGTACAGCACTGTTGAAGAAAGCCCTCTCCCTGCTAGTCAAGAGAGGCA	4403
OY	4084	GCTTGACATAGAGGTTCAAGTTCAAACCCCTGAGACACACAGTACTTCAAAACAGCAGACT	4143
Db	4404	GTAATGACCAAAATTCAGTTTCAGACTCTGAGGCATCTTACCTCTAACAGCGGTGCA	4463
OY	4144	GTGGAAGAGGTCAAT-----AGAAAGGTTGTGATTTACAGACACAGTGAAAGTCCAG	4197
Db	4464	GAGAGAGAAAGGCTTAGAGAAAGTGCACAATTTTAGAAACAGTGAAAGCTTGGAG	4523
OY	4198	TGTTAGTGTGACACATTAATACAGCTGAGAAAGTCTCTGCACAGGGTGGCCACTGACAT	4257
Db	4524	CTCTGACAGTCAATATTAGTTTCGGAAGGAAGAAATCTCGAAGAAAATTAAGACTTTGCC	4583
OY	4258	CTTGACATGCAGAGGACAGGTACCCCTGGGGCCCTGAGTCTCAGGACGAATCCATCCA	4317
Db	4584	GCTCATCCAGGGGAAGATGCTGTGGCCACAGGGCCCGAGTGTGCABGCAAAATGCACACA	4643
OY	4318	ATTCATGTAACCTCCTGCTCTGAAAGCACCCATACATCTGACCTTACAAGAGAAATTAAGC	4377
Db	4644	GTGTATGATATCTGCTATCTACCAAGAAAGGCTTAAGTTCGCAGACTGGAAGAGAGAAAGCC	4703
OY	4378	GCATCCAGAGAGAGGCATCAGAGAGGAAGGACAGCCAGATGCTGTGATGATGCTAC	4437
Db	4704	ACATCATCTGAAGTGAAGTCAAGTGAAGTGCATGAGCAGAGTTGCTTGC-----AGGAG	4757
OY	4438	GGCAGAGAGACTACAGCAATCGAAAAAGTCTCAAGGCTGAACCTGAGATCCTGAAACT	4497
Db	4758	GTCAAAATGATGTAGCAATG---AGGATTTAGAGCCCTGAAGAAATGGGATTTTGGAACTT	4814
OY	4498	GAGAGTAAAGCAAAAGATTTGTGTCAGTCGTCATTTGACAGAGCCGTTGACCAGTTGCCA	4557
Db	4815	GAGAGCAAAAGCGATAAATTGTTCACAAAACATATCTACACAGCGCGTTGACCAGTTGTA	4874
OY	4558	CGTAC---AGAAACAGCCCCGCAACTCATGCTTATGATTCACACACAGCCAGTTCTGCA	4614
Db	4875	CGTACAGAAAGAACAGCACCGGAAATGTGAGCTGTGAGTTTACACACAAAGCTCACAGTG	4934
OY	4615	TGCAGGCTTACAGCAGGGA 4634	
Db	4935	ATTAAGACTGACAGCCAGGA 4954	

RESULT 5  
US-09-880-107-3439  
Sequence 3439, Application US/09880107  
Patent No. US20020142981A1  
GENERAL INFORMATION:  
APPLICANT: Horne, Darci T.  
APPLICANT: Vockley, Joseph G.  
APPLICANT: Scherff, Uwe  
APPLICANT: Gene Logic, Inc.  
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer  
FILE REFERENCE: 44921-5028-WO  
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; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3439
; LENGTH: 6608
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 U81607
US-09-860-107-3439

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Query Match	37.4%	Score 1945.6	DB 10	Length 6608
Best Local Similarity	67.5%	Pred. No. 0	Mismatches 134	Indels 243
Matches 3253	Conservative	0	Mismatches 134	Indels 243
Oy	1	ATGGCGCAGAGGAGTGTCCACGAGCAGCGAGGACCCCGGACACCGCGC---	GGGGAGCGAC	57
Db	192	ATGGCGCGCGGGAGGTCCACCGAGCAGCGCAGCCCGGAGCAGCCCGCAGGGGAGCTCC	251	
Oy	58	ACGCCGAGCGAGCTGGTCTCAGTGGCCATGGGCCCGCAGCTGAAGCCTCGGGA-----	111	
Db	252	ACGCCGGGTGAGCCCGGAGCCCGAGCGGGCGGCCCTCGCGCGAGGGCGCGCAGACACC	311	
Oy	112	---GGAGCTGGAGAGACCCCGCAGCCCGGACCCCGGACCCCGCAGCTCCACAGAAATGGC	168	
Db	312	ACCGCGGAGACCCCGCATGCTGCTGGAGCCCGCGCACCAACCTCTTCAGAAAGATGGT	371	
Oy	169	CAGCTGTCTTCTGTCAACGGCGCTACTGTGAACAGAGATGTCTCATGTCCAAAGAGAAAC	228	
Db	372	CAGCTGTCCACCATTAATGGCGTACTGTAGCAAGATGAGCTCAGGCTCAGGAGGGTGAC	431	
Oy	229	CAGGAGGG-----	246	
Db	432	CTAAATGGCCAGAAAGAGACCCCTGAACGGTCAAGAGGCCCTTAAACAGCCAGGAGAGAA	491	
Oy	247	GAAGTCGTTGATGAGATGTTGGACAGGAGGAGTGAAGATGTGAGAGAAAGACCGA	306	
Db	492	GAAGTCATTTTTCACGAGAGTTGGACAGAGAGACTTGAAGATGTAGCGCAAAAGAGACTCC	551	
Oy	307	GTTGAAGAATGGCGCCCACTCCACAGCTGTTGAAGATATCCAAAGAGATGGCAGAGAG	366	
Db	552	GATAAAGATGGGTACTAATAGTCACAGCGTGTTCACAGATCAAGATGATGGCAGAGAG	611	
Oy	367	GAGACATCAGAAATATTTGAACAGATCCCTGCTTCAGAAACATGTGGAAGAAATGCTA	426	
Db	612	GAGA---ACCGAAATATGGAACAGATCTCTTCTTCAGAAAGCAATTTAGAAAGCTAACCA	668	
Oy	427	CAGCTGCTGATGCCAGAGCTAATGATTTGGCTTCAGAAAGATTTTAAATTTTGTGT	486	
Db	669	CAACCCACTGATGCCAGAGCTTAATATTTGATTTTAAAGAGTCTTTTAAAGTTTGTGGC	728	
Oy	487	TTTTAATTCACAGGTGCAAGAGATTTAAATGAAAGTACAGTACTGTCCAATACTCACT	546	
Db	729	TTTTAATTCACGTGTGAAAGAGATTAAGACAGAGAGACCTGACACGTCTCAGCTACTCACT	788	
Oy	547	GTCAGAGAGATGAAGGCGAAGGGCAGAGAGCTCTGTGCGAGCTGAGAGCCACGAGAG	606	
Db	789	GTCAGAGAGATGAAGGCGAGGAGACACCA-----GGGGCTGGGAGACCACGAGAGC	839	
Oy	607	CCGAGTGGGAGACTGGCGTGGAGAGTCAAGATCCAAAGAAAGAGACTGAGAAATCC	666	
Db	840	CCCGACCTTTGGGGCT-----GGAGAGCGATCTCCAAAGAAAGGAAACCCCAAAATCT	893	
Oy	667	ACAGAGAGCAAGAGGACACCTGAGAGCAGAGAACAGACAGCAGAAATCCCCCTTAA	726	
Db	894	ACAGAGAAACCCGAAAGAGACCTTGAAGGCTAGAGCAAAACGACGAGAAATTTCTCCCCA	953	
Oy	727	GCCGATCTGATCAGCGGCTGAGAGAGAGCCAAAGATGAAGGAGAAAGAAACAGAG	786	

Db	954	GCGCCAATCTGGCCAA --- GCAGTGGAGGAATGCAAAAGAGGAAGGAAGGAAGAAACAAAGAA	1010
QY	787	AAAGAGCCACCAAGTTCGCCAGATCCCGAGACAGCCAGTCACAGTGGACACATCT	846
Db	1011	AAAGAACCTTAGCAAGTCTGCAGAAATCTCCGACTAGTCCCGTACGACGAAGAAACAGATCA	1070
QY	847	TTCTTTCAAGAAATTTCTTCACTCAGGTTGGGCGCGGTGGCCGAACAACAGCATCTCAAG	906
Db	1071	ACCTTCAAAAAATTTCTTCACTCAAGGTTGGGCGCGGTGGCCGAAAAAACCAAGTTTCAGG	1130
QY	907	AAATCAAAAGAGATGATCTGGAATCTGCCGGAAGAGAAAGACACAGAGGACGACAAAA	966
Db	1131	AAAGCCAAAGAGAGATGAATGGAGAACTTCAGAGAGAAAGAAAGAACACAGACCGACAAAAA	1190
QY	967	GTAGACGAGAGAGAAAAAGAAAAAGACAGCCAGCCTCGAGAG- -----	1010
Db	1191	GTAGACACAGAAAGAAAGACGGAAGGACGAGTTGGCTCCGAGAAACTGACCGCTCCGAG	1250
QY	1011	-----GCAGAGCCGCGAGAAAGACACAGACAGACCGCAGGTTCTCAGCAGACTAC	1059
Db	1251	CAGGCCACCCACAGAGAGCCGCGAGAAAGTGCACAGACAGCCCGGTTTATCAGCTGAATAT	1310
QY	1060	GAGAAAGGTGAGAGCTCCTTTGGAAGACCAAGTGGTGGATCTGGAGACATCTCAGAGAG	1119
Db	1311	GAGAAAGTTGAGCTCCCTTAGAGAGAGCAAGTCAGTGGCTCGCAGAGACCTTTGGAAGG	1370
QY	1120	AAGTGTCTCTCTTTGGCCACGGAAGTGTTCATGAGAGATGGAAGCCACCAAGAA- --	1176
Db	1371	AAACCTCTCTCTGTTGGCGACAGAAAGTTCATGAGAAATATGAAGTCCACCAAGAAAGAG	1430
QY	1177	GTTTTCACAGAGGTCACGTGACACCGTGGAGAAACAGAGAGAGACAGAGAGAGAGAGGA	1236
Db	1431	GTTTGTGGCCGAAGTCCACGTGACACCGTGGAGAGAGAAACCGAAGACGAGAAAC- --	1486
QY	1237	GGAAGAGCTGAAGGGGGCGGTGGTGTAGAAAGAAACGAGAAATCTTCCGCCCTTGAGAA	1296
Db	1487	-----GGAGGTGGAGAAACAGCGGGTCTGTGCGCACTGTAGAA	1526
QY	1297	CTGGCTGAGCCCGAGAGGTCCCCACAGAAAGCTGACCTGCTGAGAGAGCTGTGAAGAGC	1356
Db	1527	TTGGTGAATGATGATGACGAACCTCAGAGAAAGCCGAACCTGCCAAGAGCTGGTGAAGCTC	1586
QY	1357	AGAAGATGTGTCTCTTGGAGAGACACACTCAACTACAGACTTAAGTCTGAAAGG	1416
Db	1587	AAAAAAGCTGTGTTTCCGAGAGAGACCTTACACAGAGAGCTGACCTCAGTCTGATAG	1646
QY	1417	AAGAGCGTCCCAACACCCAGAAAGCATGTACAGAGAGTGGAGATGCTGCTCCTGAG	1476
Db	1647	AAGTGTCTTCCAAACCCCGGAGAGCGTTGTGATGAGAGGTGGAATGTGTCTATCACAG	1706
QY	1477	GAAAGAAATCAGGTACAGGGGAAGTCCCTTGAAAGAACTTTCAGTAGTCAAGCTTAAAG	1536
Db	1707	GAGAGAAATGAAGGTCAGGGGAAGTCCACATTAAGAAAGCTTTTACACGACATGGCTTAA	1766
QY	1537	AAGTGTCTGGGAAGACGAAGAGGGGAACAGAGAGTGGGGAGACGAGAGACCTTGA	1586
Db	1767	AAGCTTCTGGAAGAAACAGAAAGGGAAGAAAGGAG- --GGAAGAGACGAGGAATCAGGG	1833
QY	1597	GAAATCAACACATTCACACCGAATCCCAAGAGAGTGTGATAGACAGAGAGAGAGAGC	1656
Db	1824	GAGCACACTAGTTTCCAGCCGATTTCTCCGACAGCCAGAGAGAGCAAAAGGCGAGAGC	1883
QY	1657	TCTGCTGTCTCCCGAGAGAGCTGTAGAGAGACAGCTGTCTGTGGAGAAAGGCGCGTGA	1716
Db	1884	TCTGCTGTATCCCTGTAGAGAGCCCGAGAGATACGTGTCTGGAAAAGGCTTAACCGAG	1943
QY	1717	GCACCCAGATGGGGAAGCTGAGGAAGGAAGTACTTCCGATGGAGAGAGAGAGAGAA	1776
Db	1944	GTCGACAGAGATGGGGAAGCTGAAGAAAGGAGCTACTTCCGATGGAGAGAGAAAAAGAGAA	2003
QY	1777	GGGATCACTCCCTGGGATCTCTTCAAAAGATGTATACACCCAAAGAAAGGCTCGAAGA	1836
Db	2004	GGTGTCACTCCCTGGGATCTCTTCAAAAGATGTATACCCCAAGAGGCTGTGTGACGG	2063

Oy	1837	CCCTCTGAGAGTACAAAGAGAGAGAGCGTCGAGAGGTCAAGAGCCGACCTTGTCCGC	1895
Db	2064	CTTTCGGAAAGTGATTAAGAAAGTGAAGTCGGACAAAGGTCAAGAGCGCTACTTGTCTTC	2123
Oy	1897	ACTATATGACACAGTGTCTAGAAATATGCAAAGATGAAAGTCAAAACTGTTGTGTGAGGAACAAAG	1956
Db	2124	ACGAGAGACAGAGCTCTGTAAATATGCAAAGAAATATGAAAGGAGCGTGTGAAGAGCCAAAG	2183
Oy	1957	CCAGAGAACCCAAAGCGTAGGGTGATACTTAAAGTCTTGGGAAGCACTATTTGTGTCT	2016
Db	2184	CCGGAAACACCAAGGCCAAGGTGGATACCTCAGTATCTTGGGAAGCTTTAAATTTGTGTG	2243
Oy	2017	GGATCATCCAAAGAGAGAGCAAGAGAGCATCTCTTCCAGATGATGAGAGAGGCGCAAGG	2076
Db	2244	GGATCATCCAAAGAAAGAGCAAGCAABAGTCTCTTGTGATGAGAGAAAGGGGGACCAAAA	2303
Oy	2077	ACACTGGAGGGGACAGTCAAGAGCAGAGAGAGGCCAGCAAGAACAAAGAACCCGGAGCA	2136
Db	2304	GCAATGGGAGAGAGCCACCAGAAAGCTGATGAGGCCGGAAAAAGCAAAAGAACCGGGGACA	2363
Oy	2137	GAGCGTTCCTGTGCGACAGCACCCAGAGAGAGAGAACCAAGGCCCAAGAAAGTTCCACCCGAG	2196
Db	2364	GAGCGGATCTTGTGTGTTCTCCAAAGAACATGATCCAAGGCGAAGGAAATTTCTCCCGGAG	2423
Oy	2197	CCAGCGGGAAGCCCTTCCGAAGGGGAAAGGTGTCTCCACTTGGGAGTCATTTAAAGATTA	2256
Db	2424	CAAGCTGGAAGCCCTACCGAAGGGAGGGCGGTTCACCTGGAGATCTATTTAAAAAGTTA	2483
Oy	2257	GTCACGTCCAAAGAAAAAATCCAGTCAATAAACCTGGAAAGAAAGCCGAGAC-----	2307
Db	2484	GTCACGCCAAGAAAAAATAAAGTCCAAAGCTGGAAGAGAAAGCAAGACCTCATAGCT	2543
Oy	2308	---TCTAGTGTAGAGCAGTTGTCTCACTGTGAGATCGAACCCAGTAGAGAAATCTTGGGTT	2364
Db	2544	GGGTCTGGTGTAGAGCACTTCCACTCCAGACCTGAACCCCGTAAAGAAATCTCGGGTC	2603
Oy	2365	TTCATTTAAGAAATTCATCCCGGACGGGAAAGAAAGGGCGAGACGGAGCAAGAACAA	2424
Db	2604	TCAATCAAGAAATTTATTTCTGTGACCAAGAAAGAAAGGCCAGATGGGAAACAAAGAACAA	2663
Oy	2425	GCCACTGTGGAAGCTCAGGGCCAGTGTGAGATTAATGAGAGACGACCTTAATGTCCACACC	2484
Db	2664	GCCCTGTGTAAAGCGAGGGGCCAACAGGGGCCAACAGAAATGACTCTGTATGTCCCGGCC	2723
Oy	2485	GTCGTGCTGTGTCTGAGTATTAATGCAAGTGTGAGAGGGAGAGATGG-----AGCC	2535
Db	2724	GTTGTCCCTCTGTGTGATGTATGCTGTATGAAGAGGGAATAATATGAGGACACAGCAACC	2783
Oy	2536	CAGGGGAATACGGAGCGGCCCCAGCTGTGGGGGCGTGTACTGTCTCGAGAGAGCTCAGT	2595
Db	2784	CAAAAAAGCGAGAGCGACGCCAGCGACGAAGAGCAGCCACTGAGGTGTCCAAGAGCTTCAGC	2843
Oy	2596	AAGACTGTGTCACACTGTGAGTGTGTGCAAGTCAATGATGGAGGACCAAGGCAAGTCAACCAGT	2655
Db	2844	GAGAGTACAGTTTATATGATGATGAGCAGCAGCTGTGCTGACGAGGAGCAAGGCGACGTACATTT	2903
Oy	2656	GTCGAAGAGCGGTCTCTTGTGTGGATATCCGCTCCGTATACGAAGACCTTTGATGACACACA	2715
Db	2904	ATTGAACAAAGCTCTCTTTTGGATATGTGCTTCAGTGTACAGAACTCTTTGAACAACTA	2963
Oy	2716	GCGGAGAGAGCATGCGCACCTGTTTGAAGAGAGTCACTGAAAGAAAGACATATATGC---AGAA	2772
Db	2964	GAACTGAAAGCCGACCTGTTAATCTGAGAGAGTATTTGGAAAGAGAAAGTAAATTTGCAAGAAATA	3023
Oy	2773	GAAACTCTGTGTCAACCCAGACGTTAACAGAGCGTTAAAGATGCCATATGACACATGCTC	2832
Db	3024	GAAACCCCCACAGGTATGTAACTGTCCAGAGAAACAGAGAGGCCCGGAGGCGACACGCTC	3083
Oy	2833	ACCGATGAAGTGAATTCACCTCGAAGAGCTGTACAGCCGACAGAGACGCTCAAGAGCTCTGC	2892
Db	3084	GTTATGTAGAGGGGAATTGACCCCGAAGCTGTGTACAGCTGTGCAAGAAATTCGACAGGCGCATTTG	3143

QY	2893	CGTACTGAAAGAAAGTTTACCAGAAAGCATCGGGGGCCGGAAGAGAACCCACAGACATGGTGTTCGCCA	2952
Db	3144	GGTTCGCCGAAGAAAGAACCCGGAAGCATCTGCTGCTGGAAGAGAACCCACAGAAATGGTGTTCACACA	3203
QY	2953	GTTTCCCGACGTGACTGTACCTCCCCAGACACACAGAGAAAGCCACCCAGTTAGAGAGSTA	3012
Db	3204	GTTCTCCCACTTAAACCGACTCCCAAGACACCACAGAGAGAGCCACTTCGGTGCAGAGAGGTG	3263
QY	3013	GAGAGTGGTGTGCTAGATTACAGAAAGAAAGAGAGCGCCAGACCGCAGGCCATCTCTCCAGACC	3072
Db	3264	GAAGTGGCGCTACTGACTACATAGAAGCAAGAGAGCGGAGCTCAAGAGGTCTCTCCAGGCA	3323
QY	3073	GTTCCAGACAAAGGTGAAAGAGAGAGTCCAGAGTCCCTGCACAC---CAGACTGTGCAGAGA	3129
Db	3324	GTCGCAGAAAAAGTGAAGAGAGGAAATCCACACTCTCCGAGACCGGTGGGCGCAAGAAATGTG	3383
QY	3130	ACGGGCTCAAAAAGCACATGGAAGAGTGTGAGAGAGTGTGAGAGAGACTCCGAAAGTGGTGGCT	3189
Db	3384	CTTCAGGCTGTGCAAGAGACAGAGGCCAGAAAGACCAGAAAGACAGGCTGAAGCGTGGGT	3443
QY	3190	TCGGAAGAAAGAAAGAGACGTTATGTCGAAAGAGACCCGTCAGAGAGCTGAGAGCTAGCAT	3249
Db	3444	CTGAAGAAAGAGAGCGATGTAGTGTGGAAGATGATGTCAGAGAGCAAAAACCTAGGCT	3503
QY	3250	CTTGACACAGGCTCTTGAGACTGCACAGGCTACTCCAGAGACCTTGG--AAAGTCTCTGAA	3306
Db	3504	TTTACACAAAGGGAAGGTGGTGGGGGAGACCACCCCGAAAGCTTTGAAAAAGCTCTCA	3563
QY	3307	GTCACGGCAGATGTA-----GACCAATGTGGCCAGCTGCCA-----	3341
Db	3564	GTCACAGAGACATATAGTGTCCAGTGAAGCTTTGTAACTGTGCAAGCCGAAACCTTAGCT	3623
QY	3342	--GGTTATCAAGCTTCACGAGCTGATGGAAGAACAGCCGTCGCCCTGAGCATCCGAAAC	3399
Db	3624	GGGGTAAATATACAGAGAGATGATGATGGAACAGGCTATCCCTCGACTCGGTGGAAAC	3683
QY	3400	TTTGACAGACAGTGAAGACAAATGGAAGACTCCCTTGACAGATTACAGACACTGCAGATGG	3459
Db	3684	CCTACAGACATGTGACTGTATGGAACACCCCGTACCGCATTTTGAGCGACCAAGACACA	3743
QY	3460	ACACAGCAAGATGAAACCATTTGACAGCGACGAGAGTAAGAACCACTGACGCTGCAGGAG	3519
Db	3744	ACCCAGAAAGACAGATTTGTGAAATTCATAGAGAGATGAGCTGCACATGTGTGCCAG	3803
QY	3520	TCACAGGTCACAGAAAGAGAGGCGGCTACTGCTCAGAAAGAGAGCTCTGCACACTACT	3579
Db	3804	TCAGGGGGCACAGAAAGCAGAGGCAAGTTCCTGCACAAAGAAAGAGGCTCTCAGCACTCC	3863
QY	3560	AATATATGTTCCAGCCACAGAGAAACATGGGGAAAGAACCGAAGAGATGTTCTTGAACCT	3659
Db	3864	AGTTTGTGTTCCGAGAAAGAACTAAAGAAACAATCAAAATGGAAGACACTGTAGCAT	3923
QY	3640	ACACAGCAAGAGCTTACTGCTGAGCGCGTCCGCTCTGGCAACATCAGATGGTGGCTAA	3699
Db	3924	ACAATTAAGAGGTGTCAAGTGGAACTGTATTCATTCTGTCAAAACACTGAGGGGCTCAA	3983
QY	3700	GAGGGTGA-----GCTTGACGTGGTTGATGTGAGAAAAGTCAAAAGAAACAGAGAG	3750
Db	3984	GAGGCTGACAGTATGCTGATAGAAAACCAAAAGACGTACATTTTTCGAAGAGACTTGA	4043
QY	3751	GTTGTTTGTACTACTGTG-----ACCCAAACGTCAAAAGGCTGCTGATGTGACATATGAC	3804
Db	4044	GGGTCTATTAGACACAGGCATATMACAGTCACTCGGAAAGAGTCACTGAGATGGTCCCTTAA	4103
QY	3805	AGTGAAGTAAAGGAGTGGCGCGGGGTGTCAGAGAAAAGAGAGTACAGATGCAAGG----	3860
Db	4104	GGTGAAGGACAGAGAAAGCTTGATGTAAAGAAAGATGATGCTTGTGAACCTGAGAGTCA	4163
QY	3861	-----TCTTACCCTGAGAGAGAGAGATGGAATCAGACTGATGAAAAAGAGAAA	3909
Db	4164	GCTAAGTCTCTCATCTCCCGCGTGGAGAGAGAGATGTGTTCAGTGCAGAAAGAGAGAAA	4223
QY	3910	AGGAGACAAAGCCACGACAGATGAGTGAAG--AAAGTGAAGCAAGAAACCGCGTCTCT	3966

Db	4224	ACAGAGAGAGGCCAACCCATGTGAAAGAGAGAACCTTGAGGACGAAACACCTGTTAC	4283
OY	3967	GAGCATGAGGAACCTCAGGGAGCCAGTCTCGACACTTGACATGGCCGACGTACAGAG	4026
Db	4284	GTAATCTGAGACGGTCACTAAGCAGCTCTCCAGACAGTGAATGTGCCATTCATTAATGGG	4343
OY	4027	GGGAAGGCACCTGGGAAGCCTTGGAGGAAAGCCCTTCTC-----TCCAGACCACAAACCA	4083
Db	4344	GCAAAAGGAAGTCACACATTTGGGAAGGAGGCCCTCTCCCTGCTAGTCAAGAGGAGCA	4403
OY	4084	GATTGCATAGAGTTTCAAGTTCAAAGCCTGGACACAAACAGTCACTCAAACAGCAGAGCT	4143
Db	4404	GTATGACACAAATTCATTAAGTTTCAGAGCTCGAGGCATTCATCTTAACACAGCGCTCA	4463
OY	4144	GTGAAAAAGTCAT-----AGAAAGGTTGTATTTCAGACACAGGTGAAGTCCAAAG	4197
Db	4464	GAGGAGGAAAAAGCTTAGAGAAACCTGCACACATTTTAGAAAACAGGTGAAAACGTTGGAG	4523
OY	4198	TGTGTAGGTGCACCTTATTACCAAGCTGAGAGTCTCTGCAACGGGTGGCCACTGAGCT	4257
Db	4524	CCTGAGGTGCACCTTAGTATTGTTCTGGAAAGAAATCCTGTGAAAAAATGAAAGCTTGGCC	4583
OY	4258	CTTGACATGACAGAGACAGCAGGTACCCCTGGGCTCGATCTCAGGACAGAAATCCATCCCA	4317
Db	4584	GCTCATCCAGGGGAAGATGCTGTGCCACAGGGCCCGCATGTCTAGGCAAAATCGACACCA	4643
OY	4318	ATCATAGTAACCTCTGCTCTGAAAGCACCCCTACATCTGACCTACAAAGAGAAATAAGC	4377
Db	4644	GTGTAGTATCTGCTACTTACCAGAAAAGGCTTAAGTTCGACCTGGAAGAGAGAAACC	4703
OY	4378	GCATCCACAGAGAGGCATATGAGGAAGAGACAAACCAGATGCTGTCTGATCTTAC	4437
Db	4704	ACATCACTGGAAGTGAAGTATGATGAAGTGAAGACAGAGCTGTCTGCC-----AGAG	4757
OY	4438	GGCAGAGGAGATACGAAATCGAAAAAGTCTCAAGGCTGGAACCTGAGATCTCTGGAATTT	4497
Db	4758	GTCAAAAGTGAAGTGAAGCAATTTG---AGATTTTAGACCTGAAAATGGGATTTTGGAACTT	4814
OY	4498	GAGAGTAGAGCAACAAGATTGTGTCTGAAGTCATTCACAGACAGCGTGAACAGTTCCCA	4557
Db	4815	GAGACCAAAAGCAGATAACTTTGTCCAAAACATATCCACACAGCGTTGACCAAGTTTGA	4874
OY	4558	CGTAC---AGAAACAGCCCCGAAACTCATGCTTATGATTCAACAGACCCAGGTTCTTSCA	4614
Db	4875	CGTACAGAAAGAACAGCCACGAAATGTTGACGTGTGATTTACAGACCAAAAGCTCACGTG	4934
OY	4615	TGCAGGCTTGACACAGAGGGA	4634
Db	4935	ATAAAAGCTGCACGCCAGGA	4954

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? RESULT 6
? US-10-101-487-74
? Sequence 74, Application US/10101487
? Patent No. US20020169125A1
? GENERAL INFORMATION:
? APPLICANT: LEUNG, DAVID W.
? APPLICANT: BERGMAN, PHILIP A.
? APPLICANT: LOFOUJIST, ALAN
? APPLICANT: PIETZ, GREGORY E.
? APPLICANT: TOMPKINS, CHRISTOPHER K.
? APPLICANT: WAGGONER, JR., DAVID W.
? TITLE OF INVENTION: RECOMBINANT PRODUCTION OF POLYANIONIC POLYMERS AND USES
? TITLE OF INVENTION: THEREOF
? FILE REFERENCE: 077319/0329
? CURRENT APPLICATION NUMBER: US/10/101,487
? CURRENT FILING DATE: 2002-03-20
? PRIOR APPLICATION NUMBER: 60/277,705
? PRIOR FILING DATE: 2001-03-21
? NUMBER OF SEQ ID NOS: 116
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 74

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RESULT 8
US-10-101-487-71
; Sequence 71, Application US/10101487
; Patent No. US20020169125A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, DAVID W.
; APPLICANT: BERGMAN, PHILIP A.
; APPLICANT: LOFOUIST, ALAN
; APPLICANT: PIETZ, GREGORY E.
; APPLICANT: TOMPKINS, CHRISTOPHER K.
; APPLICANT: WAGSONER JR., DAVID W.
; TITLE OF INVENTION: RECOMBINANT PRODUCTION OF POLYANIONIC POLYMERS AND USES
; FILE REFERENCE: 077319/0329
; CURRENT APPLICATION NUMBER: US/10/101,487
; PRIOR FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/277,705
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 71
; LENGTH: 522
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: CDS
; LOCATION: (1)..(522)
US-10-101-487-71

Query Match          1.7%: Score 89.6; DB 9; Length 522;
Best Local Similarity 50.2%; Pred. No. 2.6e-13;
Matches 221; Conservative 0; Mismatches 219; Indels 0; Gaps 0;

QY 905 AGAATCAAAAGAGATATCTGAAACTGCCGAGAGAAGAAAGCAAGCAGAGAAA 964
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DB 5 AGGAAGAGGAAGAAAGAGGAAGAAAGAAAGAGAAAGAAAGAAAGAAAGAAAG 64

QY 965 AAGTGCAGCAGGAAGAAAGAAAGAAAGACAGACCGCTCGAGAGACAGAGCGCCAG 1024
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DB 65 AGGAAGAGGAAGAAAGAGGAAGAAAGAAAGAGAGAAAGAAAGAGAAAGAAAG 124

QY 1025 AAGACACAGCAGGCGCAGGCTGTCTCAGCAGACTACGAGAAGGTGAGCTCTTTGGAG 1084
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DB 185 AGGAAGAGGAAGAAAGAGGAAGAAAGAAAGAGAAAGAGAGAAAGAAAG 244

QY 1145 TGTTCATGAGAAAGATGGAAGCCCAAGAAAGTTGTTCAGAGGTCCACGTGACACCG 1204
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DB 245 AGGAAGAGGAAGAAAGAGGAAGAAAGAAAGAGAAAGAGAGAAAGAAAG 304

QY 1205 TGGAAACACAGAGAGAGAGCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1264
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DB 305 AGGAAGAGGAAGAAAGAGGAAGAAAGAGAGAGAAAGAGAGAGAGAAAGAG 364

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DB 425 AGGAAGAGGAAGAAAGAGAG 444
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RESULT 10
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; Sequence 69, Application US/10101487
; Patent No. US20020169125A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, DAVID W.
; APPLICANT: BERGMAN, PHILIP A.
; APPLICANT: LOFOUIST, ALAN
; APPLICANT: PIETZ, GREGORY E.
; APPLICANT: TOMPKINS, CHRISTOPHER K.
; APPLICANT: WAGSONER JR., DAVID W.
; TITLE OF INVENTION: RECOMBINANT PRODUCTION OF POLYANIONIC POLYMERS AND USES
; FILE REFERENCE: 077319/0329
; CURRENT APPLICATION NUMBER: US/10/101,487
; PRIOR FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/277,705
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 73
; LENGTH: 530
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: CDS
; LOCATION: (1)..(530)
US-10-101-487-73

Query Match          1.7%: Score 89.6; DB 9; Length 530;
Best Local Similarity 50.2%; Pred. No. 2.6e-13;
Matches 221; Conservative 0; Mismatches 219; Indels 0; Gaps 0;

QY 905 AGAATCAAAAGAGATATCTGAAACTGCCGAGAGAAGAAAGCAAGCAGAGAAA 964
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DB 526 AGGAAGAGGAAGAAAGAGGAAGAAAGAAAGAGAAAGAGAGAAAGAGAAAGAAAG 467

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DB 466 AGGAAGAGGAAGAAAGAGGAAGAAAGAAAGAGAGAGAAAGAGAGAGAAAGAAAG 407

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DB 406 AGGAAGAGGAAGAAAGAGGAAGAAAGAAAGAGAAAGAGAGAAAGAAAG 347

QY 1085 ACCAGGTTGTGACCTCGAGGCATGTCAGAGAGAAAGTGTCTCTTTGGCAAGGAG 1144
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 346 AGGAAGAGGAAGAAAGAGGAAGAAAGAAAGAGAAAGAGAGAAAGAGAAAGAAAG 287

QY 1145 TGTTCATGAGAAAGATGGAAGCCCAAGAAAGTTGTTCAGAGGTCCACGTGACACCG 1204
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DB 286 AGGAAGAGGAAGAAAGAGGAAGAAAGAAAGAGAGAAAGAGAGAAAGAGAAAGAAAG 227

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DB 226 AGGAAGAGGAAGAAAGAGGAAGAAAGAAAGAGAGAGAGAGAGAGAGAGAGAAAG 167

QY 1265 AAGGAACAGAGAAATCTTGGCCCTCGAGAAATCTGCTGAGAGAGAGAGAGAGAG 1324
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QY 1325 AAGCTGAGCCTGCTGAGAG 1344
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DB 106 AGGAAGAGGAAGAAAGAGAG 87
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RESULT 9
US-10-101-487-73/c
; Sequence 73, Application US/10101487
; Patent No. US20020169125A1
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RESULT 11
US-10-101-487-106
: Sequence 106, Application US/10101487
: Patent No. US20020169125A1
: GENERAL INFORMATION:
: APPLICANT: LEUNG, DAVID W.
: APPLICANT: BERGMAN, PHILIP A.
: APPLICANT: LOFOUJIST, ALAN
: APPLICANT: PIETZ, GREGORY E.
: APPLICANT: TOMPKINS, CHRISTOPHER K.
: APPLICANT: WAGGONER JR., DAVID W.
: TITLE OF INVENTION: RECOMBINANT PRODUCTION OF POLYANIONIC POLYMERS AND USES
: TITLE OF INVENTION: THEREOF
: FILE REFERENCE: 077319/0329
: CURRENT APPLICATION NUMBER: US/10/101,487

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RESULT 12  
 US-09-864-761-20733  
 Sequence 20733, Application US/09864761  
 Patent No. US20020048763A1  
 GENERAL INFORMATION:  
 APPLICANT: Penn, Sharon G.  
 APPLICANT: Rank, David R.  
 APPLICANT: Hanzel, David K.  
 APPLICANT: Chen, Wensheng  
 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
 TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY  
 FILE REFERENCE: Aecomica-X-1  
 CURRENT APPLICATION NUMBER: US/09/864,761  
 CURRENT FILING DATE: 2001-05-23  
 PRIOR APPLICATION NUMBER: US 60/180,312  
 PRIOR FILING DATE: 2000-02-04  
 PRIOR APPLICATION NUMBER: US 60/207,456  
 PRIOR FILING DATE: 2000-05-26  
 PRIOR APPLICATION NUMBER: US 09/632,366







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; SEQ ID NO 336
; LENGTH: 100
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-728-445-336

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Query Match	1.2%	Score	64.4	DB	10	Length	100
Best Local Similarity	87.2%	Pred.	2.9e-07				
Matches	82	Conservative	0	Mismatches	11	Indels	1
						Gaps	1

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**Db**      1 TGACAAGAAGATGTTCACGTCCAAGAGGAAGCCAGAGTTGGCGAAGAGCAAGAAGTCAAC 60

Search completed: December 10, 2002, 00:43:39  
Job time : 1733 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

## OM protein - protein search, using sw model

Run on: December 9, 2002, 21:27:58 ; Search time 39 Seconds  
(without alignments)  
1204.077 Million cell updates/sec

Title: US-08-978-277A-4

Perfect score: 8073

Sequence: 1 MGAGSTFQRPSEOPAGSDT.....AMAPRKCLPRLQIKAPYSK 1596

## Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

## Database :

Issued\_Patents\_AA:\*  
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2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep:\*  
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6: /cgn2\_6/ptodata/2/1aa/Backfill1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5421.5	67.2	1346	2	US-08-635-121-2
2	4274.5	52.9	1780	1	US-08-769-309A-5
3	4274.5	52.9	1780	1	US-08-994-570-5
4	952.5	11.8	292	1	US-08-769-309A-3
5	952.5	11.8	292	3	US-08-994-570-3
6	656	8.1	651	1	US-08-769-309A-17
7	656	8.1	651	3	US-08-994-570-17
8	639.5	7.9	453	1	US-08-769-309A-14
9	639.5	7.9	453	3	US-08-994-570-14
10	521.5	6.5	396	1	US-08-769-309A-15
11	521.5	6.5	396	3	US-08-994-570-15
12	462	5.7	1786	4	US-08-973-462-8
13	388	4.8	1805	1	US-07-853-913-2
14	365.5	4.5	3696	4	US-09-134-001C-5080
15	361.5	4.5	2101	1	US-08-466-380-4
16	361.5	4.5	2101	1	US-08-470-950-4
17	361.5	4.5	2101	1	US-08-467-781-4
18	361.5	4.5	2101	2	US-08-483-924-4
19	361.5	4.5	2101	4	US-09-452-294-1
20	361	4.5	2137	4	US-09-134-001C-4463
21	358.5	4.4	2101	1	US-08-195-487-4
22	358.5	4.4	2101	5	PCT-US93-06160-4
23	354	4.4	1618	1	US-07-853-913-4
24	354	4.4	2409	6	5180808-2
25	334.5	4.1	1162	2	US-08-728-323A-2
26	334.5	4.1	1162	2	US-09-298-568-2
27	334	4.1	1018	1	US-08-072-610-2

28	334	4.1	1018	2	US-08-719-822B-2	Sequence 2, Appli
29	334	4.1	1018	4	US-09-092-458-2	Sequence 2, Appli
30	321	4.0	1852	1	US-08-425-061-24	Sequence 24, Appli
31	321	4.0	1852	2	US-08-825-886-24	Sequence 24, Appli
32	321	4.0	1863	1	US-08-425-061-16	Sequence 16, Appli
33	321	4.0	1863	1	US-08-480-784-2	Sequence 2, Appli
34	321	4.0	1863	1	US-08-483-553-2	Sequence 2, Appli
35	321	4.0	1863	1	US-08-487-002-2	Sequence 2, Appli
36	321	4.0	1863	1	US-08-483-554B-2	Sequence 2, Appli
37	321	4.0	1863	1	US-08-488-011B-2	Sequence 2, Appli
38	321	4.0	1863	2	US-08-825-886-16	Sequence 16, Appli
39	321	4.0	1863	4	US-08-850-727-2	Sequence 2, Appli
40	321	4.0	1863	5	PCT-US95-10202-2	Sequence 2, Appli
41	321	4.0	1863	5	PCT-US95-10203-2	Sequence 2, Appli
42	321	4.0	1863	5	PCT-US95-10220-2	Sequence 2, Appli
43	320	4.0	1898	1	US-08-056-200-94	Sequence 94, Appli
44	320	4.0	1898	4	US-08-800-644-94	Sequence 94, Appli
45	319.5	4.0	1939	4	US-09-310-187A-1	Sequence 1, Appli

## ALIGNMENTS

RESULT 1  
US-08-635-121-2  
; Sequence 2, Application US/08635121  
; Patent No. 5910442  
; GENERAL INFORMATION:  
; APPLICANT: Gelman, Irwin H.  
; TITLE OF INVENTION: TUMOR SUPPRESSOR GENE  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond  
; STREET: 30 Rockefeller Plaza  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10112-0228  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/635,121  
; FILING DATE: 19 APRIL 1996  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clark, Richard S  
; REGISTRATION NUMBER: 26,154  
; REFERENCE/DOCKET NUMBER: A30558 - 165/33603  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-408-2558  
; TELEFAX: 212-765-2519  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1346 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHEICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: Internal  
; ORIGINAL SOURCE:  
; US-08-635-121-2  
Query Match 67.2%; Score 5421.5; DB 2; Length 1346;  
Best Local Similarity 91.6%; Pred. No. 0;

Matches 1098; Conservative 24; Mismatches 62; Indels 15; Gaps 7;

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Db 1 MEAHGEVAEVSVYVTEKTEEGGGEAGGVEGTEGSESLPEPKLAPPOVPOEAPBA 60
OY 447 BELMSREMCVSGGDHDTLDSPEEKLPHKHEGIVSEVEMLSQERIKYVGSPLKLF 506
Db 61 BELMSREMCVSGGDHDTLDSPEEKLPHKHEGIVSEVEMLSQERIKYVGSPLKLF 120
OY 507 SSSGLKLSGKQKQKRGKGDEPEGEYOHITESPESADEKGSASSPEPETTL 566
Db 121 SSSGLKLSGKQKQKRGKGDEPEGEYOHITESPESADEKGSASSPEPETTL 180
OY 567 EKPLEAPDQGEAEGTSDGEKKRE---GITPMASFKNMTPKKRYVRPESDEKEEL 622
Db 181 EKPLEAPDQGEAEGTSDGEKKRE---GITPMASFKNMTPKKRYVRPESDEKEEL 234
OY 623 EKVKSATLSSTDSVSEMODEVKTVEGEOKPEPKRRVDTSVSWALLICVSSKKRARA 682
Db 235 EKVKSATLSSTDSVSEMODEVKTVEGEOKPEPKRRVDTSVSWALLICVSSKKRARA 294
OY 683 SSSDEGGRITGGDSHRAEASKDEACTDAVPASTODQAGSSSPREPAGSPGEG 742
Db 295 SSSDIR-GRRTLGGGQSGGQSGGQSRSTDAVPASTODQAGSSSPREPAGSPGEG 353
OY 743 VSTWESFKLTPPKRKSCKLEEK--AEDSSVQLSTEIPEPSREESVWS--IKKFIPIGRK 799
Db 354 VSTWESFKLTPPKRKSCKLEEK--AEDSSVQLSTEIPEPSREESVWS--IKKFIPIGRK 413
OY 800 KRADGQEQATVEDSGPVEINEDDPNPAVPLSEYNAREKMEAGNTELPOLLGAVY 859
Db 414 KQMGHQEQATVEDSGPVEINEDDPNPAVPLSEYNAREKMEAGNTELPOLLGAVY 472
OY 860 VSEELSKTLVHTVSAVIDGTRAVTSVEERSPSWISASTEPLEHAGMAMPVEEVTEK 919
Db 473 VSEELSKTLVHTVSAVIDGTRAVTSVEERSPSWISASTEPLEHAGMAMPVEEVTEK 532
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Db 593 DMVASVQLTSDPDTTEATPVQEVESVLDTEEEERQOAILQAVADVKKESQVAPAQ 652
OY 1040 TVOIRGSKALEVEVEEEDSEVLASEKEDVMPKGPVQAGAEHLAOGSETGATPESLE 1099
Db 653 TVOIRGSKALEVEVEEEDSEVLASEKEDVMPKGPVQAGAEHLAOGSETGATPESLE 712
OY 1100 VPEVTADVDHVAATQYIKLQQLMEQAVAPESSETLTDSESTPLADSDTADGTQODET 1159
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OY 1160 IDSQSKATAAARQSOVTEEEAATAQKEPSTLPNNVPAOEHEGEPGRDVLPTQOELT 1219
Db 773 IDSQSKATAAARQSOVTEEEAATAQKEPSTLPNNVPAOEHEGEPGRDVLPTQOELT 832
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OY 1400 CYGAHLLPPEKSSATGHTLQHAEDTVLPGPSQSAESIPIYTPAPESTLHPDLOGEIS 1459
Db 1013 CYGAHLLPPEKSSATGHTLQHAEDTVLPGPSQSAESIPIYTPAPESTLHPDLOGEIS 1072
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OY 1460 ASQRESEEDKPDAGPADGKESTAIEKVLKAEPELLELESKNKIVLNYIQTAVDQFA 1519
Db 1073 ASQRESEEDKPDAGPADGKESTAIDKVLKAEPELLELESKNKIVLNYIQTAVDQFA 1132
OY 1520 RRETAPETHAIDSOTQVPACRLDSREPNCWTMMKADAKMHPVPQPRDDLOVLTYLEW 1578
Db 1133 RRETAPETHAIDSOTQVPAMRLDSREPNCWTMMKAKMHPVPQPRDDLOVLTYLEW 1191
```

## RESULT 2

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US-08-769-309A-5
; Sequence 5, Application US/08769309A
; Patent No. 5741890
; GENERAL INFORMATION:
; APPLICANT: Scott, John D.,
; APPLICANT: Nauert, Brian J.,
; APPLICANT: Klauck, Theresa M.
; TITLE OF INVENTION: Protein Binding Domains of Gravin
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower/233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/769.309A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5741890and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33451
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1780 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-769-309A-5
```

Query Match 52.9%; Score 4274.5; DB 1; Length 1780;

Best Local Similarity 57.8%; Pred. No. 9.2e-255; Matches 957; Conservative 187; Mismatches 402; Indels 109; Gaps 36;

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OY 1 MGASSTEQRSPEO--PAGSDTSESLVSGHGAARAS--GAADDPADA--DPATKLPKNG 56
Db 1 MGASSTEQRSPEO--PAGSDTSESLVSGHGAARAS--GAADDPADA--DPATKLPKNG 60
OY 57 QLSVNGVAEGQDVHVOENEGQ-----EEVVDVEDVGORESEVDYREKDR 102
Db 61 QLSVNGVAEGQDVHVOENEGQ-----EEVVDVEDVGORESEVDYREKDR 120
OY 103 VEDMANSTAVEDITKQGEETSEIIEQIPASENVNVEVQAEQANDVGKXKPFVG 162
Db 121 VEDMANSTAVEDITKQGEETSEIIEQIPASENVNVEVQAEQANDVGKXKPFVG 179
OY 163 FKFTYKDKNEKSDPYQOLLTVKKDEGEAGASVAGADHOEPVETAVGESAKESSELKOS 222
Db 180 FKFTYKDKNEKSDPYQOLLTVKKDEGEAGASVAGADHOEPVETAVGESAKESSELKOS 234
OY 223 TEKQECTLKQEOSSTEIPLQAESDQAAEEBAKDEGEKEKPEKPSPESSPVNSETTS 282
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Db      235 TEKPEETLKEQSHAEISPPAESGAV--EECKEEGEEKQEKERPSKAESPSTSVTSETGS 293
      283 SEKKFTTHMAGRRKTSKRSKSKEDDLTAERKKEDEAKVDEEKEKEEPASE-----337
      294 TRKKFTTQMAKRRKTSRKRPREDEVEASEKKKEDEPEKVTDEEKGKAVASEKTLASE 353
      338 ----OEPADTOARLSADYEKEVPLEDOVGDLSEASEKCAPLATYFDEKMEAHQ--E 392
      354 QAHQPEPAPSAHEPRLSAEYELPSEBOVSSQSPSEKRAPLATYFDEKIEVHOEE 413
      393 VVAENVHSTVEKTEEBEBOGGGGEAGGVVEGTESLPPEKLAPOEYPOEAPEAEIMKS 452
      414 VVAENVHSTVEEBTEBO-----KTEVEETAGVPAEELVGMDEAPQEAPEAKELVKL 465
      453 REMCVSGGHTQULTDLSPEEKLPRKPEGVSVEMLSQERKRVGSGPLKLFSSGLK 512
      466 KEVCVSGEPTQCADLSPEKVLSKPPEGVSEVEMLSQERKRVGSGPLKLFSTGLK 525
      513 KLSGKKOKKRGCGGDEEPEGYOHIHTESPESADECKGESSASSPEPEETTCLEKPLE 572
      526 KLSGKKOKKRR--GGDEEAGEHTQVADSPDSOEOKGESSASSPEPEETTCLEKLAPE 584
      573 APQDGEAEETGTSDEGKKREGITPMASFKKMVTPKRRVRPSESDKEEELKYKATLSS 632
      585 VOODGEAEAGATSDGEEKREGVTPMASSFKKMVTPKRRVRPSESDKEDLDKVKATLSS 644
      633 TSTYSSEMDEKVTVEEBOKPEPRKRVTSVSMELICVSGSKARAKASSDDGGR 692
      645 TESTASMEMEEMKGVSEERPEPRKRVTSVSMELICVSGSKARRSSSDEGGR 704
      693 TIGDOSHRAEASKDEAGTDAVAPASTODODAGSSPEPAGSPGEGGVSTWESFKRL 752
      705 AAGGQHQKADDEAGKKEGTDTDLGASQEHDPQOGSSSPQAGSPTEGECVSTWESFKRL 764
      753 VTPRKSKSKLEAKED---SSVEQLSTEIEPSRESVWSIKKFLPGRKKRQADKOQ 808
      765 VTPRKSKSKLEKSESDSIAGSGVHSTPDTERKKEESVWSIKKFLPGRKKRQADKOQ 824
      809 ATVEDSGPYEINDDNNVAVVPLSFYNAVERKME---AQGTETLPOLLGAVYSEELS 865
      825 APVEDGPTGANEDDSDVAVVPLSEYDAVERKMEAOQAQKAEQPEKAAAEVSEKLS 884
      866 KTLVHTVSAVADGTAAVTSVEERSPMISASYTEPLEHTAGAPMPVEVTEKDLIA--E 924
      885 EGVVHMAAAVADGTAAITIEERSPMISASYTEPLEEYEAFAALLTEVLEFREVIAEE 944
      925 EPPVLTQTLPEGKDAHDMVTSEVDTSEAVTATETSEALRTEEVTLASGAETTDMVSA 984
      945 EPPVTETPLPENREARAGDTIVVSEALTPRAVTAETAGPLGSEEGTEASAABETTEMVSA 1004
      985 VEOULTSPPTTEAATPVQVESGVLDTEEBEQTQAILDAVADKVEEQAAT-----1038
      1005 VQULTDPSPTTEAATPVQVEGVPIEQRTOEVLQAVAEKVEEQLPOTGPEDEV 1064
      1039 -QTVORTGSALEKVEVEEEDSEVLASEKEKDMAPGVQEAQEAHLAOGSEFGAATPS 1097
      1065 LQPVQQA-----EAPRPEQQAASGLKETDVVLKVDQAEAKTEPFTGKVVGOTTPE 1118
      1098 LE-VPEATADVH---VATQV-----IKLOOL-MEOAVAPESSSETLTDSETNGSTPLAD 1147
      1119 FEKAPQVTESSIELVTTQCAETLAGVKSQEVMEQAIPPSVETPDTSETDGTSPVAD 1178
      1148 SDPADSTOODENIDSDSKATAAVARSQVTEBEAATQKEEPTLPNNPAPQEHHEEFG 1207
      1179 FDPAGTTODEVEIHEENEVHLV--PVKGTAEAVPAQKERPPA--PSSVVFQDETEEQSK 1236
      1208 -RDVLEPTQOELTAAVVPYLAKEVQGEVMDLGEKVK-----EEOGVFVMSG--PNS 1259
      1237 MDOTLEHTKEKVSVEVTSILSTKEGTQ--EADQYADEKTKVDFEFGLSIDGTITVSR 1294
      1260 OKAADVTTDSEVGVAGCOEKESTEVOS-----LSIEEGEMETDVAKERETKPEOVSEE 1314

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Db      1295 EKVTEVALKGEETEAECCKDDALELQSHAKSPSPVEREMVQVEREKTEAPETHNEE 1354
      1315 G--EQETAAREHGETYKRPVLTIDMPSSERKALGSLGS--PLPPODKAGCTIEVQOSID 1372
      1355 KLEHETAVTVSEVSKQLDQTVNVPILIDAKEVSSLEGGSPPLCGEEAVCTKIOVQSS 1414
      1373 TTVTQTAEAVERKI--ETVVISSETGESPEVCYGAHLLPARKSSATGHWLLOHAEDEVPLG 1430
      1415 ASFTTLTAAAEKEEVKLGENTNILETGETLEPAGAHVLEKSSSEKNDFAHNGEDAVPTG 1474
      1431 PESQAESPIITVTPAESLTHPDLQGEISASQERSESEEDKPDAGDADKESTALEKVL 1490
      1475 PDCQAKSTPVIASATTKKGLSDLEGEKTSLSKMSKDEVEQVACQEV--KVSVAIEDL- 1531
      1491 KAEP--LLELSKSNKIYLVNQTAVDQFART--ETAPETHAVDSOTQVPAORLDSREP 1547
      1532 --EPENGILELETKSSKLVONITQVADQFVREETATEMLTSELQTAHVIAKADSQAG 1589
      1548 RCWTK-----MKDAKMKHPQOPREDLQVLTVLEA 1577
      1590 QETKEGGEERQASADEPTPITSAKEESESTAVQQA 1624

```

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RESULT 3
US-08-994-570-5
; Sequence 5. Application US/08994570
; Patent No. 6090929
;
; GENERAL INFORMATION:
; APPLICANT: Scott, John D.,
; APPLICANT: Naurel, Brian J.,
; APPLICANT: Klauack, Theresa M.
; TITLE OF INVENTION: Protein Binding Domains of Gravin
; NUMBER OF SEQUENCES: 24
;
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower/233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/994,570
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6090929and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33451
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
;
; TELEX: 25-3856
;
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1780 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
; US-08-994-570-5

```

```

Query Match      52.9%; Score 4274.5; DB 3; Length 1780;
Best Local Similarity 57.8%; Pred. No. 9,2e-255;
Matches 957; Conservative 187; Mismatches 402; Indels 109; Gaps 36;

      QY      1 MGAGSSTEBORSPEQ--PAGSDTPESELVLSGHPRAAKS--GAADPRADA--DPATKLPQKNG 56
      DB      1 MGAGSSTEBORSPEQPPGEGSTPAEBPSPGGPSAAAPPTADPAIMASDPATKLLQKNG 60

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```

;
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-769-309A-3

Query Match 11.8%; Score 952.5; DB 1; Length 292;
Best Local Similarity 66.1%; Pred. No. 2.5e-51;
Matches 199; Conservative 30; Mismatches 53; Indels 19; Gaps 4;

OY 254 KDGEEKOEKPEKPSPESSPVNSETTSFKKFPTHGNAGMKKTSFKKSKEDDLETAE 313
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
DB 1 KEEGEKOEKPEKPSASPTSPVTSETGSTFKKFTQGAGMKKTSFKRPKDEVEASE 60
OY 314 KRKEOAEKVDEBEKTEPASEE-----QEPAEIDTQARLSADYEKVELPLEDOY 364
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
DB 61 KKKEOPEKVDTEEDGKAIVASERKLTASEQAHQPEAPSAHEPRLSAEKVELPSEBOY 120
OY 365 GDLEASSEKCAPLATEVDEKMEAHQ-EVVAEVHVSIVTEKTEEOGGGGEABGVVNEG 423
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
DB 121 SGSQGPSEKPAPLATEVDEKLEVHQEEVVAEVHVSIVTEERTEO-----KTEVEE 172
OY 424 TGESLPEKLAEPQEVPOEAPAEELMKSRMGVSGDHTQLDLSPEEKTLPKHPEGIV 483
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 173 TAGSVAEELVGMADAPQAEPAKELVKLETVCSEDPDQADLSPDDEVLSKPEGVV 232
OY 484 SEVEMLSOERIKVQGSPLKLTFSSSGLKLSGKKOKGRGGGDEPEGYOHIHTESPE 543
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
DB 233 SEVEMLSOERMKVQGSPLKLTFTSGLTKLSGKKOKGR-GGDDESEGHVQPADSPD 291
OY 544 S 544
DB 292 S 292

RESULT 5
US-08-994-570-3
; Sequence 3, Application US/08994570
; Patent No. 6090929
; GENERAL INFORMATION:
; APPLICANT: Scott, John D.,
; APPLICANT: Nauert, Brian J.,
; APPLICANT: Kiauck, Theresa M.
; TITLE OF INVENTION: Protein Binding Domains of Gravin
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower/233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/994,570
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6090929and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33451
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 292 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
```

```

;
; TOPOLOGY: linear
US-08-994-570-3

Query Match 11.8%; Score 952.5; DB 3; Length 292;
Best Local Similarity 66.1%; Pred. No. 2.5e-51;
Matches 199; Conservative 30; Mismatches 53; Indels 19; Gaps 4;

OY 254 KDGEEKOEKPEKPSPESSPVNSETTSFKKFPTHGNAGMKKTSFKKSKEDDLETAE 313
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
DB 1 KEEGEKOEKPEKPSASPTSPVTSETGSTFKKFTQGAGMKKTSFKRPKDEVEASE 60
OY 314 KRKEOAEKVDEBEKTEPASEE-----QEPAEIDTQARLSADYEKVELPLEDOY 364
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
DB 61 KKKEOPEKVDTEEDGKAIVASERKLTASEQAHQPEAPSAHEPRLSAEKVELPSEBOY 120
OY 365 GDLEASSEKCAPLATEVDEKMEAHQ-EVVAEVHVSIVTEKTEEOGGGGEABGVVNEG 423
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
DB 121 SGSQGPSEKPAPLATEVDEKLEVHQEEVVAEVHVSIVTEERTEO-----KTEVEE 172
OY 424 TGESLPEKLAEPQEVPOEAPAEELMKSRMGVSGDHTQLDLSPEEKTLPKHPEGIV 483
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 173 TAGSVAEELVGMADAPQAEPAKELVKLETVCSEDPDQADLSPDDEVLSKPEGVV 232
OY 484 SEVEMLSOERIKVQGSPLKLTFSSSGLKLSGKKOKGRGGGDEPEGYOHIHTESPE 543
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
DB 233 SEVEMLSOERMKVQGSPLKLTFTSGLTKLSGKKOKGR-GGDDESEGHVQPADSPD 291
OY 544 S 544
DB 292 S 292

RESULT 6
US-08-769-309A-17
; Sequence 17, Application US/08769309A
; Patent No. 5741890
; GENERAL INFORMATION:
; APPLICANT: Scott, John D.,
; APPLICANT: Nauert, Brian J.,
; APPLICANT: Kiauck, Theresa M.
; TITLE OF INVENTION: Protein Binding Domains of Gravin
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower/233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/769,309A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5741890and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33451
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 651 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-769-309A-17
```

Query Match	8.1%;	Score 656;	DB 1;	Length 651;
Best Local Similarity	38.3%;	Pred. NO. 1.4e-32;		
Matches 191;	Conservative 80;	Mismatches 188;	Indels 40;	Gaps 17;

OY	1110	VATCVO-----IKLOOL-MQOANA	PSSSEFLIDNENSGSTPLABSDTADGFOODITDSQ	1163
Dd	6	VTTIOQAETTLAGVISOEWMHQALPRPSVET	PIBDSSETDGSSTPADDACTTGKDXIEVAIH	65
OY	1164	DSKATAVAROSQVTEBEAATAOKKEEPSTL	PNNVPADOEHGEERG-RDVLEPTOEELTA	1222
Dd	66	EENEVELHY-IVRSTEEAAVPAOKERPPA-	PSSFEVQEETKEOSKMEDTLHNTDKESVET	123
OY	1223	VPLYAKTEVGOEGEVMDLOEKXK-----	EEOGVFPHSG--PNSOKAADVTDSVMGYA	1275
Dd	124	VSLISKTIEGTO--EADQYADEKTKDYAPFB	EGLEGSLDTOTIYSREKYIEVALKGGSTEEA	181
OY	1276	GCOEKESTEVOS-----LSLEEGEMETDVE	KEREKTRKPROVSEEG-EODETAAPEHEGTYG	1329
Dd	182	ECKDDDLAEIQSHAKSPSPVEREMHYOVARE	KETEATEAPHNEDEKLEHETAVTAVSEEVSK	241
OY	1330	KPVLTLMPSSEBKALGISGGS-PSLPRODKA	CIEVOVOSLDTYTNOTAAVAYKV--	1386
Dd	242	QLLOTAVNPILIIDGAKEYVSLESGSPPCLO	GEBAVCYKTIOWOSESFITLLAAEBEKVG	301
OY	1387	ETVVISTGESPECVGANHLIPAKSSATNG	GHMTLOHAEDTVBLGESAQESIPIITVPAP	1448
Dd	302	ETANILETGETLEPACGHNVLEKSES	SEKNEDFAAHNGEDAIVPTGPCOCKSPPIVASTT	361
OY	1447	ESTLHPLOGEIASQSORESEEDDKDAGD	NADGCRSTALEVUKLAERP--LTLEESKN	1504
Dd	362	KKGSSSDIEGKRTSLMKWSDVEDVOYA	COEV--KSAVAIEDU---EPENGILLETISS	416
OY	1505	KIVANVIOTAVDOFART-ETAPETHAVD	SOTOVYPACRLDSREBNRCWK----MKDKAM	1558
Dd	417	KLYONIIQTAVDQVRTEETATAMLINSEL	TQOHVHIKADSODAGQGTREKEGSEEPQASOD	476
OY	1559	KHAPYOPREDLOJUTYLEUA	1577	
Dd	477	ETPIITSAKEESESTAVGOA	495	

RESULT 7  
 US-08-994-570-17  
 : Sequence 17, Application US/0894570  
 : Patent No. 6090929  
 : GENERAL INFORMATION:  
 : APPLICANT: Scott, John D.,  
 : APPLICANT: Nauenst, Brian J.,  
 : APPLICANT: Klauack, Theresa M.  
 : TITLE OF INVENTION: Protein Binding Domains of Gravin  
 : NUMBER OF SEQUENCES: 24  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
 : STREET: 6300 Sears Tower/233 South Wacker Drive  
 : CITY: Chicago  
 : STATE: Illinois  
 : COUNTRY: United States of America  
 : ZIP: 60606-6402  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: PatentIn Release #1.0, Version #1.30  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/994,570  
 : FILING DATE:  
 : CLASSIFICATION:  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: No. 6090929and, Greta E.  
 : REGISTRATION NUMBER: 35,302  
 : REFERENCE/DOCKET NUMBER: 27866/33451  
 : TELECOMMUNICATION INFORMATION:

```

: TELEPHONE: 312-774-6300
: TELEFAX: 312-474-0448
:
: TELTEX: 25-3856
:
: INFORMATION FOR SEQ ID NO: 17
:
: SEQUENCE CHARACTERISTICS
:
: LENGTH: 651 amino acids
:
: TYPE: amino acid
:
: STRANDEDNESS: single
:
: TOPOLOGY: linear
:
US-08-994-570-17

```

Query Match	8.1%;	Score 656;	DB 3;	Length 651;
Best Local Similarity	38.3%;	Pred. No. 1.4e-32;		
Matches 191;	Conservative 80;	Mismatches 188;	Indels 40;	Gaps 17;

QY	1110	VATQV-----IKLOO--MEOAAVAPSSSEFLDPSMNGSTPLADSDPDAGPOODETISO	1163
Db	6	VTTOAQETLAVGVSQGEVMMQOALPRPSVETPRDSEI DSTPADDACTQKDXEIVH	65
QY	1164	DSKATAVROSQVTEEBEATAVQKEEPTSLPNVPAOEHEGEEPG--RDVLEPTQOELTAA	1222
Db	66	EENFEVHLV-EVRGEAEVAAPKERRPPA--PSSSEVFQEEFKEDSKMEDTLLEHTQESVET	123
QY	1223	VPIVAKTEVGOEGEVDMLDOEKK-----EEGEVFNHSG--PNOSKADVTYDSEWGY	1275
Db	124	VSLISKEGTQ--EADQYADEKTKDVPFEGLGSLDITITYSREKVYFVALKSGTSEA	181
QY	1276	GCOEKESTEVOS-----LSLEEGEMETDVEKEREKTRPBOVSSEG-EOETAAREHETYG	1329
Db	182	ECKRDDALELOSHNAKSPSEVEREMVQVEREKTEAPRNHNEDEKLEHETAATVAVEEYSK	241
QY	1330	KPVLTLMPSERBKALGSGGS--PSLPBDKRGCSLEVOVOSLDTVPTQTAFAVYKI--	1386
Db	242	QLOLTAVNPIIDGAKEVYSLESGSPRPLCGLOEBAVYCKIYQVOSSEASFILTAAREEKVIG	301
QY	1387	ETVAVISETGESPEVCYGAHLLPAEKSSATGCMHTLOHAEDTVPLGPRESQAESIPITVPAP	1448
Db	302	ETANILETGETLEPAGNAHLYEEKSEKKNEDFAAHNGEVAVPTGPCQOKSPRVIVASTT	361
QY	1447	ESTLHPLOGEISASQREEREEDKPDAGDADGCKSTALEVYLAAPR--LLELESKN	1504
Db	362	KKGSSDLEGGKTTSLMKWSDDEVBOVACOEV--KSAVAIEDL---EPENGILLELEITSS	416
QY	1505	KIVLVNIQTAVDQFAPR--ETAPETHAVDSOTOVPAACRLDSREBNRCWT-----MKAKM	1558
Db	417	KLVONIQTAVDQVFRTEETATEMLSLQTAQNHVYKADSOADAGOTEREKEGEEPQASAD	476
QY	1559	KHPVQPREDOQLTVLEA	1577
Db	477	ETPLTSAKEBESTAVGA	495

RESULT 8  
 US-08-769-309A-14  
 : Sequence 14, Application US/08769309A  
 : Patent No. 5741890  
 :  
 : GENERAL INFORMATION:  
 :  
 : APPLICANT: Scott, John D.,  
 : APPLICANT: Nauert, Brian J.,  
 : APPLICANT: Klauack, Theresa M.  
 :  
 : TITLE OF INVENTION: Protein Binding Domains of Gravin  
 :  
 : NUMBER OF SEQUENCES: 24  
 :  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun  
 : STREET: 6300 Sears Tower/233 South Wacker Drive  
 :  
 : CITY: Chicago  
 :  
 : STATE: Illinois  
 :  
 : COUNTRY: United States of America  
 : ZIP: 60606-6402  
 :  
 : COMPUTER READABLE FORM:  
 :  
 : MEDIUM TYPE: Floppy disk  
 :  
 : COMPUTER: IBM PC compatible  
 :  
 : OPERATING SYSTEM: PC-DOS/MS-DOS

```

1      SOFTWARE: PatentIn Release #1.0, Version #1.300
2
3      CURRENT APPLICATION DATA:
4
5      APPLICATION NUMBER: US/08/769,309A
6
7      FILING DATE:
8
9      CLASSIFICATION: 435
10
11     ATTORNEY/AGENT INFORMATION:
12
13     NAME: No. 5741890and, Greta E.
14
15     REGISTRATION NUMBER: 35,302
16
17     REFERENCE/DOCKET NUMBER: 27866/33451
18
19     TELECOMMUNICATION INFORMATION:
20
21     TELEPHONE: 312-474-6300
22
23     TELEFAX: 312-474-0448
24
25     TELEX: 25-3856
26
27     INFORMATION FOR SEQ ID NO: 14:
28
29     SEQUENCE CHARACTERISTICS:
30
31     LENGTH: 453 amino acids
32
33     TYPE: amino acid
34
35     STRANDEDNESS: single
36
37     TOPOLOGY: linear
38
39     US-08-769-309A-14

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Query Match	7.98;	Score 639.5;	DB 1;	Length 453;
Best Local Similarity	40.58;	Pred. No. 8.7e-32;		
Matches 183; Conservative	69;	Mismatches 165;	Indels 35;	Gaps 16;

QY	1110	VATCV-----IKOOL-MEOAAVAPSSSEFLIDSENGSTPLADSDTADGTOQDEITDQ	1163
Db	6	VTTQGAETIAGVAGSQEVMWMOALPPBSVETPPDSEIDGSTPLADDACTGOKDEIVELH	65
QY	1164	DSKATAAVROSQVTEEEAATAOKSEESTLPPNNVPAOEHEGEBPG-RDYLEPTOELTAA	12322
Db	66	EENEVHLV-EVPRGTEAAVPAOKERPPA-PSSEVFQETEGOSKMEDTLHTRKVSJET	123
QY	1223	VPLVAKTEVGOEBEVMLOJSEKX-----EDEDVPHSG-FNSOKADYTYDSEVMGA	1275
Db	124	VSLSTKEGTO--EADQYADEKTKDVPFEGLSGSIDTITVSRRKVEVALKGGTEEA	181
QY	1276	GCOEKSETEVOS-----LSLEBEMETDVEKEKRETRKPOVSEEG-EOETAPEHEGYG	1329
Db	182	ECKDDALBELQSHAKSPSPVEREMVVOYREKRETEAPTHVNEKLEHETAVTSEESK	241
QY	1330	KPVLTLDMPSSSEKKGALSGSGS-PSLPDQKAGCILEVOSGLDTTYQTQAEVAKVI-	1386
Db	242	QLLOTVWVPIIDAKEVSSLEGSPPQLCOEBAVCTKIOVOSSEASFLLTAAAEKKYLG	301
QY	1387	ETVVISSTGSPRCVOGHHLPARKSSATGGMHTLQAEPTVVLGREGQAESPIITVTPAR	1446
Db	302	ETANILETGETLEBPAGHHVLVEKSSSEKKNEDFPAHGBEALVPTGGDCAKSTPIVTSKTT	361
QY	1447	ESTLHPDLOGETIASASORERSEEDKDPADGPDADGKESTAEIVKLAEPD--ILELSESKN	1504
Db	362	KKGLSDLEBEKTTSLKWKSDDEVDEQVACQEV-KKSAVIDL---EPENGILELEFTSS	416
QY	1505	KIVLVYQTAVNDOPAR-ETAPTAHVDSTQ	1535
Db	417	KIVONIIQTAVNDOPARETEFAETMLNSELQTQ	448

RESULT 9  
 US-08-994-570-14  
 : Sequence 14, Application US/08994570  
 : Patent No. 6090929  
 :  
 : GENERAL INFORMATION:  
 :  
 : APPLICANT: Scott, John D.,  
 : APPLICANT: Nauert, Brian J.,  
 : APPLICANT: Klauack, Theresa M.  
 :  
 : TITLE OF INVENTION: Protein Binding Domains of Gravin  
 :  
 : NUMBER OF SEQUENCES: 24  
 :  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
 : STREET: 6300 Sears Tower/233 South Wacker Drive  
 : CITY: Chicago  
 : STATE: Illinois

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1 COUNTRY: United States of America
2 ZIP: 60606-6402
3 COMPUTER READABLE FORM:
4 MEDIUM TYPE: Floppy disk
5 COMPUTER: IBM PC compatible
6 OPERATING SYSTEM: PC-DOS/MS-DOS
7 SOFTWARE: PatentIn Release #1.0, Ver
8 CURRENT APPLICATION DATA:
9 APPLICATION NUMBER: US/08/994,570
10 FILING DATE:
11 CLASSIFICATION:
12 ATTORNEY/AGENT INFORMATION:
13 NAME: No. 6090929and, Greta E.
14 REGISTRATION NUMBER: 35,302
15 REFERENCE/DOCKET NUMBER: 27666/33451
16 TELECOMMUNICATION INFORMATION:
17 TELEPHONE: 312-474-6300
18 TELEFAX: 312-474-0448
19 TELEX: 25-3856
20 INFORMATION FOR SEQ ID NO: 14:
21 SEQUENCE CHARACTERISTICS:
22 LENGTH: 453 amino acids
23 TYPE: amino acid
24 STRANDEDNESS: single
25 TOPOLOGY: linear
26
27 US-08-994-570-14

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Query Match	7.98;	Score 639.5;	DB 3;	Length 453;
Best Local Similarity	40.58;	Pred. No. 8.7e-32;		
Matches 183;	Conservative 69;	Mismatches 165;	Indels 35;	Gaps 16;

Qy	1110	VATCOV-----IKOOL-MBOAAVAPSSSELPDSENGSTPLADSDPLADGTOQDETDQ	1163
Dd	6	VTTQOAEIAGVCSQGEVMMQOALPBPSSVETPDDSETSDGSTPADPDAGCTTQKDEIVKH	65
Qy	1164	DSKATPAVRSQVTEEBEATAVQKEEPTSLPNNVPAOEEHGEERP- RDVLEPTQOELTA	1222
Dd	66	EENFEVHLV-EVPRGTEAAVPAQKEPPA-PSSFVEQETKEQSKMEDTLEHDKESVET	123
Qy	1223	VPVLAKTEVQOEGVDMLOEKN-----EEOEVPHSG--PNSOKADVYTDEVMGA	1275
Dd	124	VSLISTKEGTQ--EADQYADEKTKDVPEFEGLEGSTIDTITSREKRYEVALKGGTEEA	181
Qy	1276	GCOEKESTEVQ-----LSLEEGEMETDVEKRETKPPOVSEEG-EOETAPEHEGTYG	1329
Dd	182	ECKDDALDELQSHAKSPSPSYVEREMVQVREKTELEPHVNAEKLHEHTAVTAYSEVSK	241
Qy	1330	KPVLLDMPSSSEKGAIGSLGGS-PSLPDQKAGCILEVQOSLDTTVYQTAAVEAKVI-	1386
Dd	242	QLDTQVNAVPIIDAKEVSSILEGSPPCLOEAVCTKIQVQSEKASFLLTAAEEKVLG	301
Qy	1387	ETVAVSTEGSPCEVCAHLLPAKSSSATGCHMTLQHAEDTVLGLGSEQASPIITVTPAP	1446
Dd	302	ETANILETGETLEPAGHNLVLEKSSSEKMDPRAMGEAVLPGDQCAKSPVIVSKTT	361
Qy	1447	ESTLHPLOEETIASQORSEEREEDKDPADGPKDESTAIEFVLKAEPE--LLELEKSKN	1504
Dd	362	KKGSLDLBEKTKTLKWKSKDEVDQVACQOEY--KSAVADL---PEENGILLETKESS	416
Qy	1505	KIVLVNIQTAVDOPART-ETAPTAAYDSOTQ	1535
Dd	417	KLVONIIQTAVDQFVTRTEETATMLNLSOTQ	448

RESULT 10  
 US-08-769-309A-15  
 : Sequence 15, Application US/08769309A  
 : Patent No 5741890  
 :  
 : GENERAL INFORMATION:  
 :  
 : APPLICANT: SCOTT, John D.,  
 : APPLICANT: Nauert, Brian J.,  
 : APPLICANT: Klauk, Theresa M.,  
 :  
 : TITLE OF INVENTION: Protein Binding Domains of Gravin





```

APPLICANT: McKay, Ronald D.G.
APPLICANT: Lendahl, Urban
TITLE OF INVENTION: Nestin Expression as An Indicator of
TITLE OF INVENTION: Neuroepithelial Tumors
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millitia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/853,913
FILING DATE: 19920319
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/660,412
FILING DATE: 22-FEB-1991
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/603,803
FILING DATE: 25-OCT-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/201,762
FILING DATE: 02-JUN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/180,548
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-4641AAAA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1805 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-853-913-2

Query Match      4.8%; Score 388; DB 1; Length 1805;
Best Local Similarity 21.3%; Pred. No. 1.8e-15;
Matches 319; Conservative 233; Mismatches 543; Indels 402; Gaps 75;

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Db 773 SPEENORICKPLERENQKRLYLEENQETFYVLESNRQPLSLVEEPEQIVAPLEV 832
Qy 362 --DOVQDLEASSEKCAPLATEVFPEKMEAOEVAEVVSTVEKTEEBOGGGAEGV 419
Db 833 SQDSLGLS--AEENVQLR--YLEEDDCINKSLLE-----DKTKSLGSLERNGDS 880
Qy 420 VV-----EGTGESL-PPK-----LAPEVQEAPEAPLELKSRCMCYSGGDHQL 465
Db 881 IIPQSETOVSLRPEEDDRIVNHLEKESQEFSPRSSEEOVM--ERSLEGENHESL 937
Qy 466 TDLSP-----EKLPHKPGIVSEVEMLSOBRIVQSGPLKLSSGKRLKSGKKG 521
Db 938 SSVKEDQWESQLEKESQDSKSLSD-ESQTF-----GPKL-ENAEHLRLAQDQ-- 989
Qy 522 KRGGGDEEPGEYOHITHSPESADEQKCESSASPEPEETTCLEKPLAPOD-GEAE 580
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Qy 581 EGTSDGEKKRGGITPMASFKNMVTPK--RYRRPSEDKKEELEKYS-----ATLST 633
Db 1031 EIASLSGKENOESIVSLKE-KGIEFYKSLTEIILPLET-ABEDLERRSKIDTOEPLMST 1088
Qy 634 D---STVSEMODE---VKTGEBOKP---EPPKRYVTSWEALICVSSKKRARA 682
Db 1089 EVARETVEPPEDEPPGSLSDENRRTLTSLKESQELSLSKKNVETVEDSQOCLOYE 1148
Qy 683 SSDDGEGPRTL-----GDSHRAEASKDKDEAGTDAVPAST----- 719
Db 1149 EGIQEOHQOESLREVYKQELPSSGNQOQWEDYVKGAVGQAPLATGVTGEDKAEHLRG 1208
Qy 720 ---QEDQDQ-----GSSSPRAGSPREG---EGYSTWSEFRRLVTPKK 758
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Qy 759 SKSLEEKAEAD--SSVEQLSTELIEPSREESWSIKKFIIGRRKKRADGKQOATVEDSGP 816
Db 1262 SNEYTEREDEDRAQAGEQDSIEVTLGLEAKRTGEL-----EQEVVGLSD-P 1307
Qy 817 VEINEDDPNVPAVPLSEYNAVEREKMEAQNTLEPQLLGAAYVS-EELSKTLVHTVSYA 875
Db 1308 RHFAREALRPS--LGEBSYAKAKIOGLEPGKEPKKAGALDGLTELPKTSSEALCO 1364
Qy 876 VIDGTAAVTSVEERSPWSIASATVPLEHTAGEAMPVEVEYKDIABET----- 926
Db 1365 GHEESESMEGWESEAS-----LETSDHGSADAPQPRPETEEDEGAGQALTLAPQKLL 1418
Qy 927 -----PVLQTLPEGKDADHDMVTSE-----VDFSEAVTATETSEALRTEEVTEA 972
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Qy 973 -----SGAETTDWVSASQSLTSDPDPTTEATP---VOEVESGLVDTSEERQOAIQ 1023
Db 1472 LDQWEGRE-----SEADLGETLPDSTPLGLYLXSPASPKMDLAGFOR-----LS 1518
Qy 1024 AYADKKEE--SOVATQTVQRTGSKALEKVEVEEDSYLASEK-----EKDWPKRP 1075
Db 1519 POGDACKEDMGVAPPAQ-----GLSGPPEEEDQGHGSLDLSSEEDLGTASLLPGVP 1573
Qy 1076 VOEAGAEHLAQ-----GSETQQAIPESL--EVPVTVADVIVAT----- 1112
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Qy 1113 -----COYIKLOLMEOQAAVAPSSSETLTDSTNGST-----PLADSDTADGTQODETID 1161
Db 1632 ASGGCGKQVDIAGROGPVQESVGLMDGLRGAANPALEMYSQDSABESGSES-- 1689
Qy 1162 SODSKATAAVROSQVTEEAATAQKEEPSTLPNNVPAQEHGEBEPGRDYLEFTQOELTAA 1221
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Db 1632 KELRAEAEERIGHILOQAGLTKEBEQTCRHLLTAQVRSLEAQAHAHQQLRDLGKFQYA-- 1689
QY 1315 GEQETAPEHEGTGKPEVLTLDMP---SSERGKALG-----SLGSPSLPD 1357
Db 1690 ----TDALKSRPEQAKQQLDLSDLSLSCBEGTPLSTSKLPRTPQPDGTSVPEGPASP1 1745
QY 1358 QDKAGCIEVOVOSLD---TTVTQTAEV-VEKVIETV--VISETGESPE----- 1399
Db 1746 SQR---LPPRVESLESXYFTPIPARSQAPLESSLSDGDFLDGGRKTRRSARRRTQIIN 1802
QY 1400 -CYGAHLLPAEKSSATGGHWTLOHAEDTVPLGPESQA-----ESIPITVPAPESTL 1450
Db 1803 ITYTKKLDVEEPPDSANSSTYSTRSA-----PASQASLRATSSSTOSLARLGSPDYGNSA 1855
QY 1451 HPDLQG--EISASQRESESEEDKPDAGPDADGKESTAIEKVLKAPE-----ILEES 1501
Db 1856 LLSLPGYRPTTRSSARRSQAGVSSGAP---GNSSFYM-GTCODEPQOLDWNRKIAELQO 1911
QY 1502 KSKKIYLVNIQTAVDQFARTETAPETHAIDSQTQVPACRLDSREPNRCWTMMKDAKKHP 1561
Db 1912 R-NRVCPPHLKTCTP-----LESR-PSLSLGTITDEEMKTG 1945
QY 1562 VPQP---REDLOVLTVLEMA---QPRK-----CLPR 1587
Db 1946 DPOETLRASMOPIQIAEGTGITTRQOQRKVSLLEPHOGPGTPESKATSCFPR 1998
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Search completed: December 10, 2002, 00:19:45  
Job time : 55 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 10, 2002, 00:19:52 ; Search time 73 Seconds  
(without alignments)  
355.106 Million cell updates/sec

Title: US-08-978-277A-4  
Perfect score: 8073  
Sequence: 1 MGAGSTTEQRSPQPGASDT.....AMAQPRKCLPRLQIKAPYSK 1596

Scoring table:  
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Gapop 10.0 , Gapext 0.5

Searched: 103943 seqs, 16242309 residues

Total number of hits satisfying chosen parameters: 103943

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA:\*

1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEM\_PUB pep: \*  
2: /cgn2\_6/ptodata/2/pubpaa/PC1\_NEM\_PUB pep: \*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEM\_PUB pep: \*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB pep: \*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8073	100.0	1596	9 US-09-902-432-4	Sequence 4, Appli
2	5421.5	67.2	1346	9 US-09-902-432-2	Sequence 2, Appli
3	4294	53.2	1781	10 US-09-738-877-3	Sequence 3, Appli
4	462	5.7	1786	9 US-09-742-096-3	Sequence 3, Appli
5	429	5.3	2665	10 US-09-864-761-34248	Sequence 34248, A
6	407.5	5.0	2368	10 US-09-815-242-5635	Sequence 5635, Ap
7	407.5	5.0	2368	10 US-09-815-242-12389	Sequence 12389, A
8	388	4.8	1325	10 US-09-864-761-35612	Sequence 35612, A
9	382	4.7	1879	9 US-09-971-536-70	Sequence 70, Appli
10	377	4.7	2478	10 US-09-815-242-5816	Sequence 5816, Ap
11	377	4.7	2478	10 US-09-815-242-12967	Sequence 12967, A
12	377	4.7	3256	10 US-09-919-172-98	Sequence 98, Appli
13	368	4.6	1400	10 US-09-764-176-7	Sequence 7, Appli
14	354	4.4	1618	9 US-09-963-875-1	Sequence 1, Appli
15	351.5	4.4	617	10 US-09-864-761-36182	Sequence 36182, A
16	339.5	4.2	2139	10 US-09-727-384-6	Sequence 6, Appli
17	334.5	4.1	2344	10 US-09-815-242-12713	Sequence 12713, A
18	323.5	4.0	1884	10 US-09-785-770A-17	Sequence 17, Appli
19	323.5	4.0	1907	10 US-09-785-770A-16	Sequence 16, Appli

20	322	4.0	2310	9 US-09-991-496-120	Sequence 120, App
21	322	4.0	2310	10 US-09-874-923-120	Sequence 120, App
22	312.5	3.9	2843	8 US-08-681-219-32	Sequence 32, Appli
23	305	3.8	3158	10 US-09-815-242-12611	Sequence 12611, A
24	304	3.8	6281	10 US-09-815-242-12996	Sequence 12996, A
25	296.5	3.7	1285	10 US-09-982-091A-2	Sequence 2, Appli
26	292.5	3.6	350	9 US-10-101-487-58	Sequence 58, Appli
27	290.5	3.6	1597	9 US-09-832-292-35	Sequence 35, Appli
28	285.5	3.5	2437	10 US-09-815-242-5834	Sequence 5834, Ap
29	284	3.5	1501	10 US-09-924-154-17	Sequence 17, Appli
30	281.5	3.5	1065	10 US-09-864-761-43248	Sequence 43248, A
31	279.5	3.5	2828	10 US-09-905-129-21	Sequence 21, Appli
32	279.5	3.5	2828	10 US-09-991-630-21	Sequence 21, Appli
33	278	3.4	2076	10 US-09-815-242-5815	Sequence 5815, Ap
34	278	3.4	2186	10 US-09-815-242-12913	Sequence 12913, A
35	277.5	3.4	2025	10 US-09-815-242-5703	Sequence 5703, Ap
36	267.5	3.3	1332	10 US-09-982-091A-4	Sequence 4, Appli
37	266.5	3.3	1192	10 US-09-758-140-6	Sequence 6, Appli
38	266.5	3.3	1192	10 US-09-972-599A-6	Sequence 6, Appli
39	265.5	3.3	1192	10 US-09-789-386-2	Sequence 2, Appli
40	265.5	3.3	1192	10 US-09-893-348-23	Sequence 23, Appli
41	264.5	3.3	1043	10 US-09-946-805-4	Sequence 4, Appli
42	261	3.2	5795	10 US-09-815-242-12610	Sequence 12610, A
43	258	3.2	1907	9 US-09-832-292-39	Sequence 39, Appli
44	255.5	3.2	1776	10 US-09-841-132-179	Sequence 179, Appli
45	255	3.2	1140	12 US-10-124-557-104	Sequence 104, App

## ALIGNMENTS

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RESULT 1
US-09-902-432-4
; Sequence 4, Application US/09902432
; Patent No. US20020160002A1
; GENERAL INFORMATION:
; APPLICANT: Irwin H. Gelman
; APPLICANT: Susan G. Taken
; TITLE OF INVENTION: TUMOR SUPPRESSOR GENE
; FILE REFERENCE: A30558-A-FWC-A 070156.0597
; CURRENT FILING DATE: 2002-04-08
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: 08/665,401
; PRIOR FILING DATE: 1996-06-18
; PRIOR APPLICATION NUMBER: 08/635,121
; PRIOR FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1596
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-902-432-4

Query Match      100.0%; Score 8073; DB 9; Length 1596;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1596; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MGAGSTTEQRSPQPGASDTPELVLSGHPAAEASGAAGPADADPTKLPQKNGQLSS 60
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OY 61 VNGVAEGDVHVEENQEGEEVDEVDVGRESEDEVREKRVEMANSTAVEDITKDG 120
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DB 61 VNGVAEGDVHVEENQEGEEVDEVDVGRESEDEVREKRVEMANSTAVEDITKDG 120
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DB 121 QERTSELTIEQIPASNNNEVAVQAPAESQANDVGFKKYKFFGFKTYKKDKNEKSDYQL 180
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Db 241 LOAESDOAAEEKADGCEKOEKPEPTKSPESPSPVNSFTTSPFKFFTHGNAGMKKTS 300
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Db 301 FKSKEDDLETAERKKEOBAEKVDEBEKEKTEBPASEBOBPADTDQARLSADYEKVELPL 360
OY 361 EDOVGDLEASSEKCAPLATVYFDEKMEAHOEVAEVHSTYBKTTEBEGGGGGAAGVY 420
Db 361 EDOVGDLEASSEKCAPLATVYFDEKMEAHOEVAEVHSTYBKTTEBEGGGGGAAGVY 420
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Db 421 VGTGTSLPEKPLAEPOEAPAEELMKSRMCVSGDHTQTLTDLSPREEKTLPHKE 480
OY 481 GJYSEVEMLSOERIKVQSGPLKTLFSSSGLKLSGKKQKGRGGGDEPEGYOIHTE 540
Db 481 GJYSEVEMLSOERIKVQSGPLKTLFSSSGLKLSGKKQKGRGGGDEPEGYOIHTE 540
OY 541 SPESADBOEGESSASSPEPEPTTCLKEPPLAPODGEABEGTTSDEKKRBSITPMASF 600
Db 541 SPESADBOEGESSASSPEPEPTTCLKEPPLAPODGEABEGTTSDEKKRBSITPMASF 600
OY 601 KKMVTPKRVRRPSESDKEEELKYKSAITLSTSTVSEMODEVKYVGEOKPEEPKRRV 660
Db 601 KKMVTPKRVRRPSESDKEEELKYKSAITLSTSTVSEMODEVKYVGEOKPEEPKRRV 660
OY 661 DTSVSWEALICVSSSKKRAKASSSDDEGGPRTLGDGSHRAEASKDEAGTDVAPASTQ 720
Db 661 DTSVSWEALICVSSSKKRAKASSSDDEGGPRTLGDGSHRAEASKDEAGTDVAPASTQ 720
OY 721 EDDOAGSSSPBAGSPSGEGVSTWESFKRLVTPPKKSKSKLEEAEDSSVQLSTELE 780
Db 721 EDDOAGSSSPBAGSPSGEGVSTWESFKRLVTPPKKSKSKLEEAEDSSVQLSTELE 780
OY 781 PSREESVWISIKKFIPIGRKKRADGKOEOATVEDSGPVEINEDDPNPAVPLSEYNAVER 840
Db 781 PSREESVWISIKKFIPIGRKKRADGKOEOATVEDSGPVEINEDDPNPAVPLSEYNAVER 840
OY 841 EKMEAGNTELPOLIGAVYVSEELSKTLVHTVSAVIDGTRAVTSVEERSPSMISASYTE 900
Db 841 EKMEAGNTELPOLIGAVYVSEELSKTLVHTVSAVIDGTRAVTSVEERSPSMISASYTE 900
OY 901 PLEHTAGEAMPVEEYTERKDIIAETPVLQTLPECKDAHDDMVTSSEVPTSEAVTATET 960
Db 901 PLEHTAGEAMPVEEYTERKDIIAETPVLQTLPECKDAHDDMVTSSEVPTSEAVTATET 960
OY 961 SEALRTEEYTEASGABETTDVMSAVSOLTDSPDTBEATPVOEVESGVLDTEEEERQTOA 1020
Db 961 SEALRTEEYTEASGABETTDVMSAVSOLTDSPDTBEATPVOEVESGVLDTEEEERQTOA 1020
OY 1021 IIOAAVADKYVESQVPATQVORTGSKALEKVEVEEDESEVLASEKEDVMPKGVQOZAG 1080
Db 1021 IIOAAVADKYVESQVPATQVORTGSKALEKVEVEEDESEVLASEKEDVMPKGVQOZAG 1080
OY 1081 AEHLAAGSETGATPESLSEVPEYTVADVHVATCQVITKLOOLMEQAAVAPSSSELTJDSFIN 1140
Db 1081 AEHLAAGSETGATPESLSEVPEYTVADVHVATCQVITKLOOLMEQAAVAPSSSELTJDSFIN 1140
OY 1141 GSTPLADSTADTODDETIDSDSKATAVRSQVTEEEAATAKOEESTLIPNNPAOE 1200
Db 1141 GSTPLADSTADTODDETIDSDSKATAVRSQVTEEEAATAKOEESTLIPNNPAOE 1200
OY 1201 EHGEERGRVLEPTQOELTAAAVPVLAKTEVQOGEFVMDLDEKYKEEOEVEVHSGPNSQ 1260
Db 1201 EHGEERGRVLEPTQOELTAAAVPVLAKTEVQOGEFVMDLDEKYKEEOEVEVHSGPNSQ 1260
OY 1261 KAADVTYDSEWGVAGCQKESETEVQSLSEGBMETDYEKERETKPPQVSEEGQOETA 1320
Db 1261 KAADVTYDSEWGVAGCQKESETEVQSLSEGBMETDYEKERETKPPQVSEEGQOETA 1320
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Db 1261 KAADVTYDSEWGVAGCQKESETEVQSLSEGBMETDYEKERETKPPQVSEEGQOETA 1320
OY 1321 APHEGTYGKPYLTLDMPSESRGKALGSLGSPSLPDDOKACIEVOYQSLDTTYTQTAE 1380
Db 1321 APHEGTYGKPYLTLDMPSESRGKALGSLGSPSLPDDOKACIEVOYQSLDTTYTQTAE 1380
OY 1381 AVEKYIETVVISETGBSPCVGAHLLPAEKSSATGHWTLQHAEDTVPLGPESQAESITPI 1440
Db 1381 AVEKYIETVVISETGBSPCVGAHLLPAEKSSATGHWTLQHAEDTVPLGPESQAESITPI 1440
OY 1441 IYTPAESTLHPDLQGEISASQRESEEDKPDADGKSTAIETVLAPEITILEE 1500
Db 1441 IYTPAESTLHPDLQGEISASQRESEEDKPDADGKSTAIETVLAPEITILEE 1500
OY 1501 SKSNKIVLNIOTAAVDOFARTETAETHAYDSOTQVPACRLDSRPNRCWTMKKDAKMKH 1560
Db 1501 SKSNKIVLNIOTAAVDOFARTETAETHAYDSOTQVPACRLDSRPNRCWTMKKDAKMKH 1560
OY 1561 PVPQREDIQLVTLVLAQAOPKCLPRLQKAPVSK 1596
Db 1561 PVPQREDIQLVTLVLAQAOPKCLPRLQKAPVSK 1596

RESULT 2
US-09-902-432-2
; Sequence 2, Application US/09902432
; Patent No. US2002016002A1
; GENERAL INFORMATION:
; APPLICANT: Irwin H. Gelman
; APPLICANT: Susan G. Jaken
; TITLE OF INVENTION: TUMOR SUPPRESSOR GENE
; FILE REFERENCE: A30558-A-FWC-A 070156, 0597
; CURRENT APPLICATION NUMBER: US/09/902,432
; CURRENT FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: 08/978,277
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: 08/665,401
; PRIOR FILING DATE: 1996-06-18
; PRIOR APPLICATION NUMBER: 08/635,121
; PRIOR FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1346
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-902-432-2

Query Match 67.2%; Score 5421.5; DB 9; Length 1346;
Best Local Similarity 91.6%; Pred. No. 1,1e-229;
Matches 1098; Conservative 24; Mismatches 62; Indels 15; Gaps 7;

OY 387 MEAHOEVAEVHSTYBKTTEBEGGGGGAEGGVYEGTGESLPPEKLABPOEVAEPA 446
Db 1 MEAHOEVAEVHSTYBKTTEBEGGGGGAEGGVYEGTGESLPPEKLABPOEVAEPA 60
OY 447 EELMKSRMCVSGDHTQTLTDLSPREEKTLPHKPEGIVSEVEMLSOERIKVQSGPLKTLF 506
Db 61 EELMKSRMCVSGDHTQTLTDLSPREEKTLPHKPEGIVSEVEMLSOERIKVQSGPLKTLF 120
OY 507 SSSGLKLLSGKKQKGRGGGDEPEGYOIHITESPESADBOEGSSASSPEPEPTTCL 566
Db 121 SSSGLKLLSGKKQKGRGGGDEPEGYOIHITESPESADBOEGSSASSPEPEPTTCL 180
OY 567 EKGPLEAPQDGEABEGTTSDEGKKRE---GITPMASFKKMVTPKKRVRRPSESQKEEL 622
Db 181 EKGPLEAPQDGEABEGTTSDEGKKRE---GITPMASFKKMVTPKKRVRRPSESQKEEL 234
OY 623 EKYKSAITLSTSTVSEMODEVKYVGEOKPEEPKRRVDTYSWMBALICVSSSKKRAKA 682
Db 235 EKYKSAITLSTSTVSEMODEVKYVGEOKPEEPKRRVDTYSWMBALICVSSSKKRAKA 294
OY 683 SSSDEGGPRTLGDGSHRAEASKDEAGTDVAPASTQEDQAGSSSPBAGSPSEGBG 742
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Db 295 SSSDTR - GPRLLGGGQSOGRGQGRKSRKTDVAPASTQDQDQSSSSPEEPAGSPSEGGG 353  
 QY 743 VSTWSEFKRLVTPRRKSKSKLEEK - AEDSPYQOLSTEIIPRSREEWVS - - IKKTFPGRRK 799  
 Db 354 VSTWSEFKRLVTPRRKSKSKLEEKAGRLTVYGACCPLRSMNVKNLGPPLLRNSPDGGR 413  
 QY 800 KRADGKQEOATVEDSGPVEINEDPNVAVPLSEYNAVEREKMEAOQNTLPLLGAAY 859  
 Db 414 KQOMRQEOATVEDSGPVEINEDPDVAVPLSEYDAVEREKMEAOQNAELPSCMGCV - 472  
 QY 860 VSEELSKTLVHTVSAVIDGTRAVTSVEERSPWISASVTEPLEHTAGEAMPVVEVTEK 919  
 Db 473 VSEELSKTLVHTVSAVIDGTRAVTSVEERSPWISASVTEPLEHTAGEAMPVVEVTEK 532  
 QY 920 DIIAETPLVPTLLEGGDAHDMDVTSYDFPSAVTATETSEALRTETVEPASAEEFT 979  
 Db 533 DIIAETPLVPTLLEGGDAHDMDVTSYDFPSAVTATETSEALRTETVEPASAEEFT 592  
 QY 980 DMVSAVSQLTSPDPTTEATPVQOEVSGLDTEEBERQOALIQAVAAKVKREESQVPAHQ 1039  
 Db 593 DMVSAVSQLTSPDPTTEATPVQOEVSGLDTEEBERQOALIQAVAAKVKREESQVPAHQ 652  
 QY 1040 TVQRTGSKALEKVEEVEDSEVLASEKEKDVPKGPVQOAGAEHLAQSEGTQATPESLE 1099  
 Db 653 TVQRTGSKALEKVEEVEDSEVLASEKEKDVPKGPVQOAGAEHLAQSEGTQATPESLE 712  
 QY 1100 VPEVYADVDAVATCOVITLQQLQMLEQAVAPESSETLTDSEFNSTSLADSDTADGTCQODET 1159  
 Db 713 VPEVYADVDAVATCOVITLQQLQMLEQAVAPESSETLTDSEFNSTSLADSDTADGTCQODET 772  
 QY 1160 IDSQSKATAAAROSQVTEEEBAATQAKKEPSTLPNNVPAOEHEGSEEPGRDYLEPTQOELT 1219  
 Db 773 IDSQSKATAAAROSQVTEEEBAATQAKKEPSTLPNNVPAOEHEGSEEPGRDYLEPTQOELT 832  
 QY 1220 AAAPVYLAKTEVQGEVDMLDGEKVKEBOEVFVHSGPNSOKAADVTYDSEVMYAGCQE 1279  
 Db 833 AAAPVYLAKTEVQGEVDMLDGEKVKEBOEVFVHSGPNSOKAADVTYDSEVMYAGCQE 892  
 QY 1280 KESTVOSLSLEEGEMETDVEKEKRETKPEOVSSEGBDETPAPEHEGTYGKPVTLMDPS 1339  
 Db 893 KESTVOSLSLEEGEMETDVEKEKRETKPEOVSSEGBDETPAPEHEGTYGKPVTLMDPS 952  
 QY 1340 SERGKALGSLGSPSLPQDQKAGCIEVOVOSLDTVTVQTAEAKEVETVIVISSEGESPE 1399  
 Db 953 SERGKALGSLGSPSLPQDQKAGCIEVOVOSLDTVTVQTAEAKEVETVIVISSEGESPE 1012  
 QY 1400 CVGAHLDPREKSSATGHWTLQHAEDTVPLGPESQAESPIITVTPAPESTLHPDLQGEIS 1459  
 Db 1013 CVGAHLDPREKSSATGHWTLQHAEDTVPLGPESQAESPIITVTPAPESTLHPDLQGEIS 1072  
 QY 1460 ASORERSEEDKPDGGRPADGKESTAIKYLKAEPELLELESKSUKIYLVNIQTAVDQFA 1519  
 Db 1073 ASORERSEEDKPDGGRPADGKESTAIKYLKAEPELLELESKSUKIYLVNIQTAVDQFA 1132  
 QY 1520 RETAPETHAVDQOVQACRLDSEPNRCMTKMDAKMKHPVQPREDDLOVLTLEAM 1578  
 Db 1133 RETAPETHAVDQOVQACRLDSEPNRCMTKMDAKMKHPVQPREDDLOVLTLEAM 1191

RESULT 3  
 US-09-738-877-3  
 : Sequence 3, Application US/09738877  
 : Patent No. US20020015970A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Murray, Richard  
 : APPLICANT: Watson, Susan  
 : APPLICANT: Weiss, Stephen J.  
 : APPLICANT: Glynn, Richard  
 : TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF ANGIOGENESIS, COMPOSITIONS, AND MET  
 : FILE REFERENCE: A-69806/DJB/JJD  
 : CURRENT APPLICATION NUMBER: US/09/738, 877

[illegible]



Db	765	VTPRKSKSKLEEKSEDSIAGSVENHSPDPEPGKEEWSIKNKPIPRKRRKKRPGRQEQ	824
Qy	809	ATVEDSGPEVINEDDPNVNAVPLVSEYNAVERKME--AOCNTLPLQILCAVYSELS	865
Db	825	APVEDAGCTGANEDSDVPVAVPLSEYDAVERKMEAOQAOKGAEOQPOKATATEVSELS	884
Qy	866	KTLVHTVSVAVIDGTRATVSVEERSPSMISASYTEPLEHTAGCANRPVEEYENKIIA-E	924
Db	885	ESOVHMMAAAAADGTRATVILIEERSPSMISASVTEPLEOVBREAALLTEEVLEREVIAEE	944
Qy	925	ETPVLTOILPEGKDADHDMVTSEVDFTSSEAVTATESEALTEEYTEASGAETTDWVSA	984
Db	945	EPPTYTEPLPENREKRGTVVSEALTEPEAVTAAATAPLGSSEBETASAEFTTEWVSA	1004
Qy	985	VSOLTSDPTTEEATPVQVEESGVLDTTEEBEROTQAILQAVADKYKEESVPAT-----	1038
Db	1005	VSOLTSDPTTEEATPVQVEESGVLDTTEEBEROTQAILQAVADKYKEESVPAT-----	1064
Qy	1039	-QTVQRTSKLKEKEVEEDSEVLASKEKEDVMKGVQOENGAHLLAOGSTGQATSES	1097
Db	1065	LQPVQRA-----EAEERBEQAEASGLKKEEDVVLAKVDAQEKTEPFGKVVGGTTPES	1118
Qy	1098	LE-VEEYADVDH---VATCOV-----IKILOL-MEQAAPESSETLIDSETNGSTPAD	1147
Db	1119	FEKAPQVYESTIESSLVYTQCAETLAGKSGQEMVMEQAILPDVSVETPIPDSEIDGSTPAD	1178
Qy	1148	SDTADGTQODETTIDSQDSKATAAARQOSVTEBEAATAOKKEEPTLPLNNVPAQEEHGEERG	1207
Db	1179	FDAPGTOKDEITVEIHENEVASQSGSTGEAEPAPKERRPPA-PSSFVFOETFEKQSG	1237
Qy	1208	-RDVLEPPOQELITAAVAVYLAKTEVQGGEGEVDMLDGEVK-----EEOGVYVHSG--FNS	1259
Db	1238	MEDTLEHTDKVESVETVSIILSTEGTO--EADQVADKTKDVPFEGLGSGIDTITVSR	1295
Qy	1260	OKAADVYTDSEVMGAGOEKSTEVOS-----LSLEGEMTQVYKEKRETKPQVQSEE	1314
Db	1286	EKVTEVALKGBETEEAECKKDDALELOSHANSPPSPVEREMVQVYERKTEAPRHVND	1355
Qy	1315	G-EOETAAPREHGTYGKPVLLDMPSSERKGLGSLGGS-PSLPDQDRAGCIEVQSID	1372
Db	1356	KLEHETAVTSEVSGSKOLLQVNVPIIDQAKVSSILEGSPPCLOGEAEVCTKIQVQSEE	1415
Qy	1373	TTVYOTAAVKEVIT--ETVVISETGESEPCGAHLLPAKSSATGCGHMTLQHAETVPUG	1430
Db	1416	ASFLLTAAAEKVKVGEFANILLETGETELPEAPAHVYLEKSSSEKKNEDPAHGEDAVPTG	1475
Qy	1431	PEQOSEPIIYTPAPESLHLDLOGEISASQRESEERDEKDPADADGKRETAIEKL	1490
Db	1476	PDCQKSTPVIYSATTKKGLSDELGEKTTSLKMSXSEVDEQVAAOEAV--KYSVAIEDL-	1532
Qy	1491	KAEPK-ILELESKSNKIVLVANTQTAVOFOART-ETAETHAVDSQOTQVPACRLDSREP	1547
Db	1533	-EPENGILLETEKSKSLVQNTIIGQAVQFOVTEETATFEMLITSELQTAHVIAKDSQDAG	1590
Qy	1548	RCWTK-----MKDAMKHVPQPRDDLOVLYVLEA	1577
Db	1591	QETEKEGEPEQASADETTPITSAKKEESESTAVGQA	1625
RESULT 4			
US-09-742-096-3			
: Sequence 3, Application US/09742096			
: Patent No. US20020155441A1			
: GENERAL INFORMATION:			
: APPLICANT: DROUHE, PIERRE			
: APPLICANT: DAUBERGES, PIERRE			
: TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES			
: FILE REFERENCE: 200773USODIV			
: CURRENT APPLICATION NUMBER: US/09/742, 096			
: CURRENT FILING DATE: 2000-12-22			
: PRIOR APPLICATION NUMBER: US 08/973, 642			
: PRIOR FILING DATE: 1998-02-06			
: PRIOR APPLICATION NUMBER: PCT/FR96/00894			

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      PRIOR FILING DATE: 1996-06-12
      PRIOR APPLICATION NUMBER: FR 95/07007
      PRIOR FILING DATE: 1995-06-13
      NUMBER OF SEQ ID NOS: 29
      SOFTWARE: PatentIn version 3.1
      SEQ ID NO 3
      LENGTH: 1786
      TYPE: PRF
      ORGANISM: P. falciparum
      US-09-742-096-3

Query Match      5.7%; Score 462; DB 9; Length 1786;
Best Local Similarity 19.28; Pred. No. 4.8e-13;
Matches 325; Conservative 291; Mismatches 644; Indels 436; Gaps

QY      53      QKNGQLSSVNGVAGODVHVOENQEOG--EEVDVGVGRESDYREK---DRVE---105
      ||:|:|      |:|:|      |:|:|      |:|:|:|      |:|
DB      95      QVNGELAS-----EEVKEIIDLLEGNLTLESVDOKNLEAEADIKENILLINIEPKK 149
      ||:|:|      |:|:|      |:|:|      |:|:|:|      |:|

QY      106      -----MAANSTAYEDITKDOQ---EEISEIIEIIPASENNVEVMQPAISOANDVC 153
      ||:|:|      |:|:|      |:|:|      |:|:|:|      |:|
DB      150      NIIDLNLNNIQNSEKEQSESENQVSDLEFNELNNSVDVNGEYKENILF--ESQVNDTI 207
      ||:|:|      |:|:|      |:|:|      |:|:|:|      |:|

QY      154      FKVKFEKVFQFKYKKKKNKESDPTVOLITVKKDGECAEASV--GADHOEPSETAVGE 211
      ||:|:|      |:|:|      |:|:|      |:|:|:|      |:|
DB      208      FNSLVK-----SYQEOQHNVKEKVEESVENDDESEVENVEANVEENDGCVASSVVE 261
      ||:|:|      |:|:|      |:|:|      |:|:|:|      |:|

QY      212      S--ASKESELKOSTEKOEGTLKOE-----OSTEIPLOAESDQAEE 251
      ||:|:|      |:|:|      |:|:|      |:|:|:|      |:|
DB      262      SIASSVDSIDSIJEENAVPTVEIIVAPSVESVAPSVESVEENVEESVAENVEESVAE 321
      ||:|:|      |:|:|      |:|:|      |:|:|:|      |:|

QY      252      EAKDGEKQKQKPTKSPESSSSPVNSSETTSSFKFTFHGACHRRKTKSKKSKEDDLF- 310
      ||:|:|      |:|:|      |:|:|      |:|:|:|      |:|
DB      322      NVEESVAENVEESVAENVEEIVAPTVEIIVAPTVEIIVAPSVESVAPSVESVEENVEE 381
      ||:|:|      |:|:|      |:|:|      |:|:|:|      |:|

QY      311      -TAERKKEOEAEKDEEKEKTEPA---SEPOEPAEDTDOARLSADYAEKVELPLEDOVD 366
      ||:|:|      |:|:|      |:|:|      |:|:|:|      |:|
DB      382      SVAEENVEESVAENVEESVAENVEESVAENVEESVAENVEEL--VAPYEEIIVAPTVEI-- 438
      ||:|:|      |:|:|      |:|:|      |:|:|:|      |:|

QY      367      LEASSEKCAPLATEVPEDEKMAHQEYVAEYHSTVKTTEEOGGGGEAGGVVECTGE 426
      ||:|:|      |:|:|      |:|:|      |:|:|:|      |:|
DB      439      VAPSVESVAPSVESVEENVE--ESVAENVEESVAENVEES-----VAENVEE 485
      ||:|:|      |:|:|      |:|:|      |:|:|:|      |:|

QY      427      SLPEPKLAEPOEPOEAPEAEELKSRMCVSGGDHTQIDLSPEEKTLRKHPGIVSEY 486
      ||:|:|      |:|:|      |:|:|      |:|:|:|      |:|
DB      486      SV-----AENVEESVAE-----NVEESVAENVEESVAENV 515
      ||:|:|      |:|:|      |:|:|      |:|:|:|      |:|

QY      487      EMLSSQERIKYQGSPIKFLFSSQLKTLGCKKQKGRGGGGDEBPGYQHIIHESPSAD 546
      ||:|:|      |:|:|      |:|:|      |:|:|:|      |:|
DB      516      EIIVAPYEEIIVAPTVEIIVAPSVESVA-----PSVEESVEENVEESVA 560
      ||:|:|      |:|:|      |:|:|      |:|:|:|      |:|

QY      547      EOKGSSASSPEEP-----EEPTOLEKGPLAPODGCAEBGTTSDGKKREGITPMASF 601
      ||:|:|      |:|:|      |:|:|      |:|:|:|      |:|
DB      561      ENVEESVAENVEESVAENVEESVAENVEEIVAPTVEIIVAPT-----DEIYAP--SVY 612
      ||:|:|      |:|:|      |:|:|      |:|:|:|      |:|

QY      602      KMWTPPKKRVRRPSSDKHEEL--EKVKSATLSTDSITVSEMODEV--KTVEBQKPEPKR 658
      ||:|:|      |:|:|      |:|:|      |:|:|:|      |:|
DB      613      ESVAPS--VEESVEENVEESVAENVEESVAENVEESVAENVEEIVAPTVEIIVAP----- 665
      ||:|:|      |:|:|      |:|:|      |:|:|:|      |:|

QY      659      RVDTSVSMREALICVGSKKRRKRAKSSDDDEGPTLGGDSHRAE--ASKDKEGTDAVP 716
      ||:|:|      |:|:|      |:|:|      |:|:|:|      |:|
DB      666      -----TYEELIVAPSVESVAPSVESSEV-----NVEESVAENVEESVAENVE 708
      ||:|:|      |:|:|      |:|:|      |:|:|:|      |:|

QY      717      ASTORODAOGSSSPSPAGSSPEEGYSTWMSFKRLVTP-----RKSKSKLEEKADS 770
      ||:|:|      |:|:|      |:|:|      |:|:|:|      |:|
DB      709      ESVAVNEESVAENVEEIVAPTVEIIVAP--PTVEIIVAPSVESVAPSVESVEENVEES 766
      ||:|:|      |:|:|      |:|:|      |:|:|:|      |:|

QY      771      SVEQLSTEIEPSRESBSWVSIRKFTIPGRKKRRADKQDOA--TYEDSGPVEINDDPNVA 828
      ||:|:|      |:|:|      |:|:|      |:|:|:|      |:|
DB      767      VAENVEESVAENVEES-----VAENVEESVAPYVEIIVAPSVEE-----S 806
      ||:|:|      |:|:|      |:|:|      |:|:|:|      |:|

QY      829      VVPLSEYNAVEREKMAQNTLDPOLLGAVYVSEELKTLVHTVSAVINDGTRAVTVSE 888
      ||:|:|      |:|:|      |:|:|      |:|:|:|      |:|

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Db 807 VAPSVESVAENATNLSDNL-LSNLLGI-ETEEIKDSILNELE-----EVKE 853
Qy 889 RSPSWISASTPELEHTAGAMPVEEYVTKDIIAETPVLTOITLPG- KDAHDWYTS 947
Db 854 N----VTTILLEVEETFTASVTFSTNILEE---IDENTTNDTIEEKLIELHEMVLAA 906
Qy 948 VDFTSAVTATESEALRTEEVEASGAETDMVASVQ-----LTDSDTTEAT 999
Db 907 LENTOSEEKEKIDYI--EVEKE-----EYATLIEVEBAEKSANTTIEFENLE-- 958
Qy 1000 PVOEVESGLDTEEBERQOAILQAAVADKVEESQVPAOTVORTSKA-----LEKVEE 1054
Db 959 --NAVESNENVAENLEKINETVFNVLDKVEETVEISGESLENEMDKAFSEIPDVK 1016
Qy 1055 VEED-----SEVLASEKEKV-----MRG-----PVQ 1077
Db 1017 IQENLLTGMFRSTIETSIIVIOSEKVDLENVSSILDNIENMKEGLNKLKLENISSTEGVQ 1076
Qy 1078 EAGAHLAOG-----SETQATPESLEVPVTAADVHVATCOYIK-- 1117
Db 1077 EYTEHVEQNVYDVDPAPAKOQFLGILNAGLKEMFLEVEFKSESQVITVEELKDE 1136
Qy 1118 -LQOLMEQ--AVAPSETLIDSEFNGSTPLADSDTADGTQDETIDSDSKATAVRO 1173
Db 1137 PVOKEVEKETVSIIEEMEEIYDVLSEEEKEDLTK-MIDAVEESIFISSDSKEETESIKD 1195
Qy 1174 SQTEEAATPAQKEEPTSLPNNVPAQEHGEGRDYLE--PQOELTAAPV----- 1225
Db 1196 K---EKDVLVVEE-----VODNDDESVEKVELKKNMEELMDAVBINDITSK 1242
Qy 1226 -LAKTEVGEVGEVDMV--DEKVE-----BOEVFVHSGPNSOKRADVTYD-----SE 1270
Db 1243 LIETQELNEVEDLIDKMEKLEKALSEDSKEIIDAKDOLLEKIVEEHITTLDE 1302
Qy 1271 VAGVACQF-----KESTVOSLSLEGE---METDYEKERRET 1306
Db 1303 VVELKVEDKEIKVSDLKDLLEDILKEVKEILESEILEDYKELKTJETDILEKKEI 1362
Qy 1307 KPEQVSEGEQETAPAEHGTGYKPYLTLDPSSSE----- 1341
Db 1363 EKDHPEKFEKEBEIKDLADILKEVSSLEVEEKKLEEVHEIKEEVERHIISDAHIKGL 1422
Qy 1342 -----KQKALGSLGSPSLPDQKACIEVOVOSLDTTQTQFAEAKVETEVY 1390
Db 1423 EEDDLLEVVDLKGSLIDMLKGMELGDMK-----ESLEVTYTKLBERVES-LKDV 1473
Qy 1391 ISETGESPCVGAH-----L-----PAEKSSATGGHNTLQHA--DTVPLG 1430
Db 1474 SSALGMDQMKTRKKAQRPKLEEVLLKEVEKEEPKKITKKKVRPDIKDKPKDEI-VE 1532
Qy 1431 PESQAESITIIYTPAESTLHPDLQCEISASQRESEEDKPDAGPDAGKESTALEKV 1490
Db 1533 VEMKDEDI-----EEDVEEDIEIEDKVEDIDEDIDIGDKD---EVIDLIV 1580
Qy 1491 KAPELLELESKNKI 1506
Db 1581 OKEKRIEKVKAKKKL 1596

RESULT 5
US-09-864-761-34248
; Sequence 34248, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEOTIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
```

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; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annotmax Sequence Listing Engine vers. 1.1
; SEQ ID NO 34248
; LENGTH: 2665
; TYPE: PRF
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL034555.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 10
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 8.9
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.8
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 14
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 7.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 9.5
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 7.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 9.3
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 7.7
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 12
; OTHER INFORMATION: EST HUMAN HIT: AU117052.1 EVALUE 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: P08640, EVALUE 3.00e-10
US-09-864-761-34248

Query Match 5.3%; Score 429; DB 10; Length 2665;
Best Local Similarity 19.6%; Pred. No. 2,1e-11;
Matches 372; Conservative 270; Mismatches 755; Indels 504; Gaps 83;

Qy 9 QNSPEOPAGSD-----TPSELVLSGHGPAEASG-----AAGPDADPAT- 49
Db 301 QVSTPEPAKSDLSKLESYVMKVPKEKGLSSHEVEKEGRKLARKHLKPEOPADGVSAVD 360
Qy 50 --KLDPKNGOLSVYAGQGVHVOEENQGOEEYVDVEDVGQRESDEYREKDRVEEMA 107
Db 361 LEKLEARRKRRFSDNIKAKKQKPEYAKSSPEMDARVL-----SKQPVSSREYI---- 411
Qy 108 ANSTAVEDITKQGOETSEIILQIPASENNVEMVQPAESQANDVGFKVFVGFKFTV 167
Db 412 -----LLRGEAEARKVRKELIKRES-----KTI----- 435
```

```

OY 168 KDKNKSPTVOLLTVKKDEGEAEASVAGDHOEBSYETAVGESAKSESEKOSTEKOE 227
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 436 -----KIDRLMTVASPKOCCELASISVSGSRPSDDLQARIGELAG-----ESVENE 483
OY 228 GTLKOEQOSTEIP-----LOAESDQAAEE--AKDEGEKOEKEPTKSPSPSPVNS 278
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 484 -----VOSKKRPPSKRPOKLOLVLDODGPEREDVRKNYCSLDEETPERKSGOEKSHSVNT 538
OY 279 ET-----TSSFKKFTFHGAWGNKKTSTFKSK-----EBDLTAERK----- 315
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 539 EKKIGIDIDHTOSTYKROMBOSRRKOOMEIKASEKFGSPKQDVDEYERSLVHEGKPP 598
OY 316 -----KOEAEKVYD-----EKEKTEPASEBOEPAEDTDQARLADYEKVEL 358
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 599 QOVTDSPSKKKRMDHVOFIDICTRERNYRSSROJSEDESERTGSPSVRHSGFHD-- 655
OY 359 PLEDOVGLEASS-----BEKCAP-----LATEVFDEKMEAHQEVAAEYHVT 401
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 656 --EDIPGSPRLSLVSGPKVDEKVLPSNITVREESLKNFNPYDSRREOMADMAKIKLSV 713
OY 402 VEKTEEDOGGGEAE--GGVVEEGTESLPEKL-----AEPOEPOAEPAE-- 448
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 714 LNSEDELNRWDSQOMQODAGRPDVSFPNSTITKROSLKRSVRDLEPEGVSDSEDEGHS 773
OY 449 -----LMKSRMCVSGDHTQLTDLSP-----EKLTPKHPEIVAE 485
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 774 HSPRASALYESSRLSLRLDRREDKLERDERLSSLERKKYFSALDKITITPDTKALLR 833
OY 486 VMLSS-----QERIVQSGP-----LKLFSSSGLKLSG 516
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 834 AKSLSSREEMNSFLDWDSPFANFRNNKDKEDYDSAPRIPSWYMKKKIRTDSESKMD 893
OY 517 KKOKGRGGGGEDEGEVGHITHESPEADDEKGESSASPEEPEETTLGKRPGLAPD 576
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 894 KREDNH-----BEEDROELFASRFLHSSIFEDOSKRLHLEKKEEDSOFISRIYKGT 948
OY 577 GEAEBGTTSDGKEREGITPMAS-FKKMY-----TPKKRYRRESEDEBELEKVSATLS 631
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 949 SSGANSTT--DSIDEPVLFHSMELTRMOQKEKEKQKREYKODTENHRTPS 1005
OY 632 STDTSVSEMO-----DEVKTVGEQKPEBKRRYDTSVSMALICVSSSKKRAKAS 684
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1006 ABEKNDSELTPPSVGPSTVVTLESAPSALEKTTGDKTVEAPLV--TEETVPAVY 1062
OY 685 SDD-----EGGPTLGGDSHRAE-----ASKDKAGADAVAPQODQOAGSSSP 733
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1063 SEEAPRASPAPRV-----EQLEQVLDLPGADPRKEAA--MPAGVBE-----GSSGDQ 1111
OY 734 ----AGSPSEGEVSTWE-----SFKRLVTPRRKSKSKLEKAE--DSVE----- 773
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1112 PYLDKPPRPGASFSQAESNVDPEDSTQPLSKPAQKSEANEPKAEKPDATADAPDAN 1171
OY 774 ----QSTLEPESREESWVSIKFFIGRRKKRADGKOEQATVEDSGVEINEDDPNPAVY 830
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1172 QRAEAPESQOPASBD--LEVDPVAAKDKKPKNSKSKPPVO--AAVSVIVE--KPYT 1224
OY 831 PSEYNAVEREKMEAGONT--ELPOLIGAVVYSEELST-----LVHVSVAVIDG 880
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1225 KXSE--RIDREKIKRNSRGEAQKLELMEKERTTRTAKSNASADLHPREPSLSLST 1282
OY 881 RA--VTSV-----EERSPSWISASVTEPLEHTAGEAMPVEEYTEKDIAE--ETPV 929
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1283 RRRNVASVATMGDHNRS-----VKRPVBO-----PRVTRKRLERLQAAAV 1327
OY 930 TOT-----LPEGDADDDMYTSEVDTSEAATATETSEALRTEEYVTEAGAF--ETTD 980
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1328 PTPPRGRPPKTRRRADEEBEENAKEPAETLKPPEGWRSPRSQKTAAGGPOGKKKKNP 1387
OY 981 MSAVSQULSDPTPEAPAPVQEVESGVLDTEEBERQTAIIQAVADKYKEEQVATQT 1040
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1388 KYDAT-----REPATTEVGPQIGVKESSMEPKAAEEBESQKRRDKAGTDDKNPETAP 1442

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OY 1041 VORTGSKALEKVEEVEEDS-----EVLASEKED--VMPKGPVOEAGAEHL 1084
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1443 VE-----VYEKKPAPKBNKSKRGSRNRSLAVDKSASLKNDAVAPRGAQAQGER-- 1495
OY 1085 AOGSENG--QATPESILEVEYADVDHATQCYIKLOQMEQAVAPESSETLTDEBTNS 1142
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1496 ---ESGVVAVSPKSESQKEDLS-----SOLKSDVPDKEPEKEDVASQ 1541
OY 1143 TPLASDGTADGTQOEDTIDS-----ODSKATAVROS-----QVTEBEAAT 1183
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1542 SPEA--TQAKQMELEDAVETHAKLAESASAAVKADAPGLAPEDRDKRAHQASLTLA 1600
OY 1184 AOK---EESPSTLPNNVPAOEEN-GEE-----PGRDVLEPTQOEL--TAAVPLAKTEV 1231
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1601 AIGSIINDISGEPENFPAPPYRGESQTDLOPPAGAOALQPEEEMETDEAVSGILETBA 1660
OY 1232 GQGEVMDLGEKVEEEOGVFHSQNSKADVYTDSEVMVAGQOESESTVOSLSLE 1291
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1661 ATESSRPVNAADPS-----AGPTDTEKARGNSSETSHSVPEAKGSEVEYTLVRKD 1712
OY 1292 EGEMETDVEKEREKPEEGVSEGEQETAAPHEGTYGKRPVLTLDMPSSERKALGSLG 1351
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1713 KGRQKTRRRKRRNTKKVYA--PVESHVPESNOAG-----ESRANEGTIV--Q 1759
OY 1352 SPSLPDQKAGCIEVOVQSLDTFTYQFA-----EAVEKVIETVVISYTGSSPECVGAH 1404
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1760 HPEAPQEEK-----QSEKPHSTPQOSTDLKIPSTENSOEISVEERTPTKASVPPD 1813
OY 1405 L-----LPAKSSATGSHMTLQNAEDTVPLGPESQAESITIIYTPA----- 1445
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1814 LPPEPQPAVDEBPQARFVHSHIESDPVTPPSD--PSIPILPLPSTAAKLSPPVASGSI 1872
OY 1446 PESTLPLDQGEISASQRESEEDKPDAGPDADGKE-----STAIEKVLKAPPEILELS 1501
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1873 PHQSPPTKTENTITROEERASTPSPALRPDTKASDVOTSSSTLKIL--MPPKYVAS 1931
OY 1502 KSNKVLNVIQAVDQFARTETAPETHAYDSOTQVPACRLDSREPNKCTKMKDAKMP 1561
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1932 VISTSVTAIAEPV-----SAAPCLH-----EAPPPVDSKKP-----LEKRTAP 1972
OY 1562 VPQPRREDLOVLYLEMAQPRKCLPRLQK-----APVS 1595
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1973 VTN--NSEIQASEVLA--ADKEKAPVIAKRTITSVISRMPVS 2011

RESULT 6
US-09-815-242-5635
; Sequence 5635, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: Elitza, Olla
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27

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PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16  
NUMBER OF SEQ ID NOS: 14110  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 5635  
LENGTH: 2368  
TYPE: PRF  
ORGANISM: Staphylococcus aureus  
US-09-815-242-5635

Query Match 5.0%; Score 407.5; DB 10; Length 2368;  
Best Local Similarity 17.5%; Pred. No. 1.6e-10;  
Matches 317; Conservative 293; Mismatches 663; Indels 541; Gaps 71;

QY 47 PATKLPQKQGLSVNGVAGQGVHVOERQEOEE- EYVDEVGORESDVEKED- 101  
DB 677 PTVKPOAKODIIQAVTTTRKQO- IKSNASLQDEKDVANDKIGIKETKAKIDIDAATT 732  
QY 102 RVEEMANSTAVEDITKDOQ- EETSEI- IEOIPASENVEEMVQPAESQ 148  
DB 733 MNOVEAIKTKAIDINOTAPATTAKAAAEFEPEVVOAQIDQAPLPDITTEVVAER 792  
QY 149 AN-DYGFKKVFEVGFVKKKNEKSDTVQLT- VKKDEGEAGASVAGADHDE 202  
DB 793 INAKVSGVKAIEATTJAQDLERVKNEISKIENITDSTQTKMDAVNEVQAATARTON 852  
QY 203 PSVETAVGSASAKESLQKSTER- QEGTLKQOSTE- IPLQAESDQ 247  
DB 853 ATVSNTNEEVADAAVAAQOGHLIDIOVYKSKQEVADTKSKVDKINAIOQAKVXP 912  
QY 248 AAEEAKDE-GEEKQKEPTKSPESPSPVNESETTSFKFETGHGAGMKKTSFKSK- 305  
DB 913 ADTVEENYNTKQOIKIONS- NASTEEKQAAT- ELDTKKQEA 954  
QY 306 EDDLETAE- KRQOEAEKVDEEKERT- EPAS 335  
DB 955 RNLDAANTNSDVTAKDNGIAINOVQATTKKSDAKAEIAQKASERKATIEAMDSTT 1014  
QY 336 EEOEPRED-TDOARLSADVEKELPLEDOYGDLEASSEKCA- PLATEVFDE 385  
DB 1015 EEOQAKKDVQDAVVTAMADIDNAANTVDNAKTNEATITAITPDANVYKPAKQALID 1074  
QY 386 KMEHGEVVAEVHSTVEKTEERQGGGEGVVEGEGSLPEPKLAEPOPEAE 445  
DB 1075 KYQAQETAI- DANNCATTE- EKAAKQOVOTEKTT 1107  
QY 446 AEELMKSRMCVSGDHTQLTDLSPREKTLPKHPEGIVSEVEMLSQERIKYQGSPLKUL 505  
DB 1108 ADTAI- DGAHTN- AEVEAKNAEIAKIEAIOPART 1140  
QY 506 FSSSGIAKISGKKQKRGCGGDEDEGEYOHITF- S 541  
DB 1141 TYDNAAQATATANERKTA- TAQTOUITAEIIAANAVNNAVTOANNIEAANS 1194  
QY 542 PESADEOK-GESSAS- SPEPEETTC- EKGPLEAPQDEGEAGETSDGKREGIT 595  
DB 1195 QNDVDQAKTTGESIDQVPTYNKATAVTDAKNNITTAITDONGVPTADAGKNSIQSTQ 1254  
QY 596 PWASFEK- MVTPKRRVRPSESDEE- 620  
DB 1255 PATAVASNAKNVDQAVTQONQOIDNTGATTEKNAKADVLKAKKAYODILNQTIN 1314  
QY 621 ELEKVSATLS- STDSVSEM- QDEVKTYGEEK- PEPRRRD 661  
DB 1315 DVTQIDQAVADVQGITADTTIKDVAKDELATKAREQKALIAQFADATTEEREQAOQVAD 1374  
QY 662 TSVSW- EALICVSSKKRARKA- SSSDEGGRPT- LG 695  
DB 1375 AELTQGNONIEANQSTIDVNTAKDNAIQALIDPQASTVDKTNARALLTEMOKITEIILN 1434  
QY 696 GDSHRAEASKD- KEAGTDAVPAST- QEOQOAGSSSPPEAG 735

DB 1435 NNBTNTEKNDIGPVRAAEGLNINNAATTGDTTAKDTAVKVOQLHANPVKPPAG 1494  
QY 736 SPEEGEGVSTWESFKRLVTPRKSKSKLEKAL-DSSVEQLSTEIPEPSRESV- 788  
DB 1495 KTLADQAAAD-KTQIEQTPNNAQOEINDAKOEVDELNOAKTNIDQSSDEVVDNAVRE 1553  
QY 789 SIKKFIPIGR- KKRAG 804  
DB 1554 GKAKINAVKTFSEYKDDALAKIEAATNAKVTEDANSNASTSSIIAKAKQIAELKQTAQ 1613  
QY 805 KQOATVEDSGPVEINEDDPN- PAVVPLSEYNAVERKMEAGNTELPQ 853  
DB 1614 NVQATSKDIDIEVQIHNDLDINIDYITPGKKSATTDLYAVADQKKNISADTNATQDE 1673  
QY 854 LIGAVVSEBELTLYHTVS- VAVIDGTRAVTSVEERSPWISASY 898  
DB 1674 KQQAQOVQONQOTALEJINGVDNGVDVDDALQGAALIDALQVDAVTPKANOVIDAKA 1733  
QY 899 TEPLF- HTAGAMPVEEVTE- KDIIAEETPV- LQOTLPBGDAHDV 944  
DB 1734 EETKESIDSDQLTAEKTEALAMIKOITDOAKOGITTDATTAVEKAKAQGLEAFDNT- 1792  
QY 945 TSEVDFTSAAVTATETSEALRTEEVTEASQAETTD- MVSAYSQLTDS 992  
DB 1793 QIDSTEKOKAIELEETALDQIEAGVNDADATTEKEAFNALBILSKATEDISDQT 1850  
QY 993 DTTEEATPVQOEVSGVLDTLEEERQTAI- LQAVADKVEESQV- PATQV 1041  
DB 1851 TNAEIAI- VNSALEQKQIRNPVYKKNALIREVYNQOIEIINNADADAKKEI 1906  
QY 1042 ORTG- SKALEKVEEVEDESEVLASEKEDVMK- GPVOAGAETHAOGSE- 1089  
DB 1907 ARTDLDRTYDRADKIDKQOTNTEV- AELQNTYITAIETAYPQNDPNANDTRNGSGDND 1964  
QY 1090 TGOATPESLEVEPYTADVDHATCOVITLQOLMEDQAVAPESSETLTDSETNGSTP 1144  
DB 1965 ATANSANATPENTGQPNVTESTDNANA- DTSSTTNNQNDAAAG 2008  
QY 1145 LADSDTADGTQODETID- SODSKATAAVROSQVTEEBATTAQKEPSTLPNN- VPA 1198  
DB 2009 ETTATANSATDADANDKQOANNSSADSTNSPTMDNVTSTKPEVEST- NNGTTDKPA 2066  
QY 1199 QEEHGEPEGDVLE- PTOELTPAAVNPVLAKTEVGOBQEVMLQOEKVK 1246  
DB 2067 TEADNATPESATNNSTTATNENAPTESTATA- PTTAST- GAESSADSKONASVN 2121  
QY 1247 E-EQEVFVHSG- PNSQKADAVTYDSEVNGVAGCQKESTEVOSLSLEEG 1293  
DB 2122 DSKQNAEIVNNSAESQSTNGKVAQPKSENKAKAKKQDRDSTNGSMVESTETELPSADITEP 2181  
QY 1294 EMETDVEKEKETKPEQVSEE- GEQETAAPHESTY- KVLVILDMPSER 1342  
DB 2182 KYSSNTSKKEESTYSQTDABOHNSDPTNVAINEADSEBNVDIVSNKP- STSKPSEAK 2239  
QY 1343 GKALGSLGSPSLPDDKAGCIEVQVOSLDTVTQFAAEVKEVTEVVVISTEGSEPCVG 1402  
DB 2240 DKA- TSEDSQKADMATADTKDNOASIGATADVNNKATON- DG 2280  
QY 1403 AHLIPAKSSATGHWTLQHAEDTVPLGPES- QAESIPIVYPAPESTLHPDLQGEISAS 1461  
DB 2281 ANASPA- TVSKGSNSANQDMLVNTKTKENKANKASQOQGVN- 2321  
QY 1462 QRESEFEEDKPDAG 1475  
DB 2322 -KPKQQAKTLPDPTG 2334

RESULT 7  
US-09-815-242-12389  
Sequence 12389, Application US/09815242  
Patent No. US20020061569A1  
GENERAL INFORMATION:





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Db 652 TEN-----GORTPEFAN-----EKTSSPAEPTHEGERTPLANENTTISPAPTEMR 697
Qy 841 EKMEAGNTELPOLLGAYVSEELSKTLVHTVSAVIGDTRAVTSVEEESPWISASTYE 900
Db 698 EETANEKTPPP-----AEPTEMRRENTMENTP-----SPAQ 730
Qy 901 PLEHAGEAMPVEEVEETEDKLIABETPVLTQTLPEGKAHDMDVSEVDPTSEAVTAET 960
Db 731 PTEN--GRTPLANET-----TPSLAEPTENG-----RTPEAKETT---S 768
Qy 961 SEALRTEEVTEASGAETTDWASVOLTSDSPDTEEATPVOEVESGLVLTDEERQTOA 1020
Db 769 SSAFEPTHEARTPLANENT-----TSSP-----AEP-----TENREBTAN- 803
Qy 1021 ILQAVADVKESQVPAQVOTQORTSKALEK-----EEVEEDSEVLASKEKDVPKGV 1076
Db 804 -----EKTQPPAPTEPNR--STANEKTPPAEPTREMTANE--NTTISPAPET 852
Qy 1077 QGAGAEHL-----AGSETGOATPESELEVEYTAADVAVATCOVAKILOQLEQAVA 1127
Db 853 EHEEETPLANETKTLSPAPTEPENGERT-----FTNEKT 887
Qy 1128 PESSETLFDSEFNGSTPLADSTP---ADGTOODETTDSQDSKATAA--VROSOVTEEBA 1181
Db 888 PSSAE---PTEHGERKPLANEITTPSRAEPTHEGERIANEKATPSPAKPTHEGETTVNED 944
Qy 1182 ATQAKEEPSTLPNNVP-AQE-----EHGEERGRVLEPTQOELTAAPVPLAKTE 1230
Db 945 TTPSSAEPTENGERTPLANENTTSPTESTEHEGERTANKTTPSPAEPTE----- 994
Qy 1231 VGOESEVMDLDEKVEEVEFVHSGPNQKADVTYDESEVAGVACQOKESTEVOSISL 1290
Db 995 -----HEERTPSANEKTIIPSPAKPTHEEMTPSA-----NEMTTPSPVP 1034
Qy 1291 EGEEMETDVEKRETKREPOVSEBQETAPEN--EGTYGKVLTLDMSSRGALGSL 1349
Db 1035 TGHGKRTTLANKITLSPGPTHEGAKTTSANEKITTPSLAKPTHEGERTSPNDITTS- 1093
Qy 1350 GGSFSLPDDKAGCIEVQVOSLDTTV---TOTFAVEKIEIVVISEGESPECGAHLL 1406
Db 1094 -AAESTEHDRKTSANVTTPAPAEPIKAKRTTLAHEKA--TOVTEKSTHEPKTTS--- 1147
Qy 1407 PAEKSSATGHTLLOHAEDTV-----PLGESQAESI-----PIVTPAPE 1447
Db 1148 TTEKTRPEKPTL-YSEKTICTKGKMPV--PEKPTENGNLTTLTEIKAVKSTENE 1205
Qy 1448 STLHPDLQGEISASQRESEEDKPDAGPDADGKESSTALEKVLKAEPELLEESKNKIV 1507
Db 1206 KT-----AAVTKTIKPSVKVTGDKSLTTSSTHNTKE--VTHQVPTGSFT 1248
Qy 1508 LNVITQAVDQFARTEFAPETHAY----DSQTOVPACRLDSRPNCW 1550
Db 1249 LITSRKUSITSEATGNESHPLYNKDGSKGIGHAGOMENDSFPRAW 1295

RESULT 9
US-09-971-536-70
; Sequence 70, Application US/09971536
; Patent No. US2002015976A1
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Havukkaia, Ilkka
; APPLICANT: Bloksberg, Leonard
; APPLICANT: Lubbers, Mark
; APPLICANT: Dekker, James
; APPLICANT: Christensson, Anna
; APPLICANT: Holland, Ross
; APPLICANT: O'Toole, Paul
; APPLICANT: Reid, Julian
; APPLICANT: Coolbear, Timothy
; TITLE OF INVENTION: Lactobacillus rhamnosus Polynucleotides, Polypeptides and Methods
; TITLE OF INVENTION: Using Them
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; FILE REFERENCE: 1043c2
; CURRENT APPLICATION NUMBER: US/09/971,536
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: U.S. No. US20020159976A1 09/634,238
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: U.S. No. US20020159976A1 09/724,623
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: PCY/N201/00160
; PRIOR FILING DATE: 2001-08-08
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 70
; LENGTH: 1879
; TYPE: PRT
; ORGANISM: Lactobacillus rhamnosus
US-09-971-536-70

Query Match 4.7%, Score 382, DB 9, Length 1879;
Best Local Similarity 19.1%, Pred. No. 1.6e-09;
Matches 324; Conservative 302; Mismatches 726; Indels 342; Gaps 70;
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Qy 20 TPESELVSGHGAFAASGAGDPADADPATKLPQ-KNQLSSVNGVAEOG--DVHGOEE 75
Db 124 TATERAKQKQGVAAEATKAKAALDOAQETEGVQARDAGIAIDAOHOPGTGLNREEA 183
Qy 76 NQEGQEEV---VDEVDGQRESEDEVREKDRVEEMANS--TAVEDITKQGOEETSETIE 129
Db 184 KQALDAEAKVTALIEIDBSTLATSEKAQKQGVADAEAKAKATAID-----QAOTILEID 237
Qy 130 Q-----IPASENVEENV-QPAESQANDVGKKYVK 159
Db 238 KAKDDGIAIDAOHQAGDFDTRKAQAKDAIDAEAKYKDAIDOPTLTAKKTKQK--Q 295
Qy 160 FYGFKETVYKDKNEKSDPVQTLTVKKDEG--EGAEASVGAGH--QEPSVEPTAVESASK 215
Db 296 GVDDEATKAKTAKTIDAKTIDGVYQAKDQGIKALIDHOQGTDLATRKOSAKALDAEAK 355
Qy 216 -----ESELKOSTEKO-----EGTLKQOSSTEIPLOASDQAEBAEANDE 256
Db 356 ITDAINODTLSTERKDAQKQAVANDEAAKAKAALDOAQNADAI-LQAOADGIKALDAHQ 414
Qy 257 GEEKQKEPTKPESSPSSPVNSSETTSFKEKFTTHGMAGKRTKTSFKSKEDDLTAERK 316
Db 415 IGADLDTOKTAKQA---IDKEAA---KVL-----ALIDOPTLTLSARK 453
Qy 317 EGEAKVDEEKEKTEPAESEGEPAEDPQO--ARLSAD-----YKVELPLEDOVGDE 368
Db 454 AQKQGVADETAKATAIDS-----ARNADELAKAQAADGIKALDAQHRIGMDLAKKRTAQ 508
Qy 369 ASSEKCAPLATEVDEKMEAHQEVVAEVHSTVEKTEEO--GGGGEAEGGVVE--- 422
Db 509 AALIDAEAKVGAALIDOPTLTLSQEKAAQKQFVALETKAKTIDAKAQAADGVYQAEKGI 568
Qy 423 -----GTGESLPPEKLAEOEVPOEAPAEELKSRKMCVSGGDHNO--LTLSPPE 472
Db 569 QALIDGHOSGALLDTRKYDAKKAIDAEAKALINDAIDOVTLTSARKAQKQKVTDEAVKA 628
Qy 473 KTLPRHPEIVSEVEMLSQERIKVQGSPLKLTFSSSGKTKLSGKKQKRGGGGDEEP 532
Db 629 KT-----AIDAAKNADIVDQAKASGLOAIDAIVHOSG-TLLDTRKQDAK--AIDAEV 678
Qy 533 FY-----QHITHSPESADQKGESSASSPPEPTECTLEKGPLAPDQGEAEETGSD 587
Db 679 KYIAAIGDVTTLQAEKLTQQAVALDANQ-----AKAALDAKNADIVDQAKADG 729
Qy 588 EK-----KREGITPWPASFKNVTPKKRYARPSSESDKEELEKVKSA---TLSSTSTV 637
Db 730 IKAIDAQHOAGL---ALNKRKEAAKLLI-----AETADKVQAALIGDVTTLTATOKAV 778
Qy 638 SEMQEVKTVGEEQ-----KPEEPKRRVDTSVSMELILCVGSSKKRARRAS 683
Db 779 QROAITVEVTKANQALIDAGNADAVDAOKNAGVKAIFYDHOSGOAL---ADRRKDAK-Q 833
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Db 1110 TTADAADAHTNAEVEAKKRAIAK--IEAIOPAT-----TTKD-----NAKE 1151
QY 603 MYTFKKRVRRSESDKEKELEKVKSATLSDTSYSEMODSVKTYGEQKPEEPKRRVDT 662
Db 1152 AIAFKAMERKAIKOTOTITAEETAANADVNAVTQANNSIEANSONDVDAQTGGEN 1211
QY 663 SVSWEALICVGSRRKRAKASS-----DDEGGPRTLGGDSHRAEASKDKENGTD-- 713
Db 1212 SI--DQYTPYVKKATANEITAILNNKLGIEIQATP-----DANDEKQADAEANTGEN 1264
QY 714 ----AVPAST--QEQDOAQSSSPPEAGSPSEGSVSTWESFKRLVTPR--KKSFKLE- 764
Db 1265 KANOAISATTNAAOVDEKAKANA-----EAAINAVPKVYKKAQKAKDEI 1307
QY 765 EKADSSVLEOLTELEPERESVSIKKFIPIGRKKRADGQEQEATVDSQVPEINEDDP 824
Db 1308 DQLOATQTNVNNQONNATTEKEKAI-----QOLATA-----VTDAKN 1345
QY 825 NVPAVPLSEYNAREKMEAGNTELEFOLLGAVYSEELSKTVHTVSVAVIDGTRAVT 884
Db 1346 NITAA---TDNGVDAQKADAKNSIQSTQPAFAVSNKKNVDQAVTQONQAIQNTTGAT 1402
QY 885 SVBERSPWISASVTEPLEHTAGEAMPVEVEYTEKDIIAETTPVLQTLPGKD-AHDDM 943
Db 1403 TEE-----KNAKDLVLEKAKERAYODIINAQT--TNDVTOIKDQAVADI 1444
QY 944 VTSEVDFTSEAVTATESEALRTEVEVTEASGAETTDMSAV-----SOLDSPTPEEA 998
Db 1445 QGITADTTIKVAADELTKRAMEQALIAQTADATTEKEKANOQVDAQLOQNONINIA 1504
QY 999 TPVOEVESGLDTEEBERKOTAI--LQAVADKVEESQVPAQTQVORTGSKALEKEVEE 1056
Db 1505 QSIDVNTA-----KDNAIOAIDPIQASTD-VKTNAFAELLEMQ-----NKITEIL 1550
QY 1057 EDSEVLASEKEDVMPKQPVQEGACAEHLAQSGSEIGQATPESLEPVEVADYDHAQCOYI 1116
Db 1551 NNNETNEKEKNDI--GPVRAAYEEGL-----NNINATTTGDTYJAKDTAVQ 1596
QY 1117 KLOOLMEQAV-APESSELTLDSENGSPPLADSPDADSTQOD-----ETISQDSKATA 1170
Db 1597 KVQOLHANPVKPKAKKELDQAAADKQTQI--EOTPNASQOEINDAKQEVTELNQATN 1654
QY 1171 VROSOVTEEEEAATAQKEEPTPLPNNVPAQEEHGEERGDLPTQOELTAAAVPLAKTE 1230
Db 1655 VDQSS-FNEYVDNAVKEGAKI-NAVKTFSEYKKD-----ALAKIE 1693
QY 1231 VGQGEVMDLGEKV-----KEQEVFVHSG----- 1256
Db 1694 DAYNAKVAEADNSNASTSSEIAEAKOKLAEIKQATADQNVNQATSKDDIEVOIHNDLNIN 1753
QY 1257 ----PNSOKA-----DVTYDSEVMGVAGQKESEYOSL----- 1288
Db 1754 DYTTPGKKESATIDLYAVAOQKNNISADTNATODEKQOAIKOVQOVQJALAESINNGV 1813
QY 1289 -----SLEGEEMETDYEKEREKRETPPE-----QVSEGEQETAPEHEGTGKRVLTLD 1336
Db 1814 DNGVDALDQOGKAIDAIDQVDAVYKPRANOAIKVAEDTKRESIDQSOQ----- 1862
QY 1337 MPSSERKALSLGSGPSLPPQDKAGCTEVQVOSLDTTVTQTAEVER-----VITTV 1389
Db 1863 LTAEEKTEALAMI--KOITQOAKQGI-----TDATTTAA-VERAKAQGLEAFAPNI 1909
QY 1390 VISETGEPEPCVGAHLPAEKSSATGCHWTLQHAEDTVPLG-----PESQASFI 1438
Db 1910 QIDST-----EKQKAE--ELETALDQIEAGVNNNAQATTEKEKEFTNAL 1952
QY 1439 PIIVTPAPESTLHPDLQELISASQERSESEEDKPDAGDAGKESTALEYKLAKEPIL- 1497
Db 1953 EDLISKATEDISDQTNNEIATVKNASALEQJLAKQRIINPEVKNALAEAREVNNQIEIITK 2012
QY 1498 --ELESNSNKIVLVNIQTAVDOFARTEETAPETHAVDSOTQ---VPA 1538

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Db 2013 NADADASAKETIARTDLGRYFDRFADKLDKTQTNNAEVAELQNTTIPA 2058

RESULT 11
US-09-815-242-12967
; Sequence 12967, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12967
; LENGTH: 2478
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-12967

Query Match 4.7%; Score 377; DB 10; Length 2478;
Best Local Similarity 18.3%; Pred. No. 3.6e-09;
Matches 305; Conservative 274; Mismatches 625; Indels 462; Gaps 68;

QY 47 PATKLPQKNGQLSSVNGVAGQDVHVOEENQGEF-EVDEDVYQGRESEVREKD---- 101
Db 681 PTVKPOAKQDIIQAVTTFKQO---IKKSNASLQDEKDVANDKIGKLETKAIKIDIAAT 736
QY 102 RVEEKAANSTAVEIDITKQGEETSEIIQIPASNNVNEEMVQRPESQANDGFFKVFV 161
Db 737 NAOVEAITKAIINIDNOTTPATTFAK-----AAALEPDEVVOAQOIDQ----- 779
QY 162 GFKFTVKKDKNKSQDVOLLTVKKDEG-EGAASVAGADHOEPEVETAVGESASESELK 220
Db 780 --PLNPDTTNEVAEALIERIAAKVSGKALEATTNAD-----LEKKNKEISKIEINT 832
QY 221 QSTE-----KQEGTLKQESST-----EIPLOAESDQAAEBEAKDEG----- 257
Db 833 DSTQTKMDAVNEVQOAVARAKQANATVSNATNEV---AADVAAQKQGLHDIQV 888
QY 258 EKEKEKPTKSPSPSSPVNSETSSFFKFFTHWAGKRTKSKSKEDELTAERKE 317
Db 889 KSKQEVADTKS--KVLDKINAIQT-----QAKVPADDEVENAVYTRK 930
QY 318 QE-----AEKDEEKEKTEPEASEQEPADTDQARLSADYEKVELPLEDQVGLSEASE 372
Db 931 QEIQNSNASTTEKQOATTELDTKQKEAKRTLDANINS----- 970
QY 373 EKCAPLATEVFEDEKMEHQEVAEIVHVSVEKTEEBEGGGGGAAGVVGEGTGSLEPEK 432

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Db 971 -----VTTAKONISIAINOVOAATTKKSDAKAEIAOKA---SERKTAIEMNDSTTEBO 1021
OY 433 LAEPOEPOEAEP-----BEIMKSRMCMVSGDHTOLT-----LSPEKTLPKPREGI 482
Db 1022 QAKKDVDAVYANADINDINAANNV-----DNAKTTNEATIAITTPDANKPAAKQAI 1076
OY 483 VSEVEMLSQERIKVQGSPLKLESSLSSGLKLSGKKOKRGGGGEGPEGOHIHTEEP 542
Db 1077 ADKVQ---AOE-----FAIDGNSNGSTTEKKAOKAQOYTER 1109
OY 543 ESADDEKSSASSSPPEPETTCLEKPLEAPODGEAEETGTDGKKREGITPMASFKK 602
Db 1110 TTADADAIDAHTNAEVAAKKAIAK--IEAIOPAT---TTTD-----NAKE 1151
OY 603 MYTPKRRVRPSEDEKEELEKVSATLSTDSVSEMDEVTVGEEOKPEPKRRVPT 662
Db 1152 AIATKANEKTAIAOTODITAEIIAAANDVDNAVYQANSINIEAASQNDVDOAKTTGEN 1211
OY 663 SVSWEALIVGSSKKRARRASS-----DDEGPRTLGGDSHRAEASKDEAGTD-- 713
Db 1212 SI--DOVTFYVNNKATARNETITAILNNKLOEIOATP-----DATDEKQAADEANTENG 1264
OY 714 ----ANPAST--QEOOQAGSSSPRAGSPSEGEVSTWSEFKRLVTPR--KKSCKLE- 764
Db 1265 KANQAIISAATTAQAQDEAKANA-----EALINAVTPPVYKKQAQAKDEI 1307
OY 765 EKAEDSSVQLSTEIPSRSESVSIKFTIPGRKKRKGADKQOATVEDSGPEIENDDP 824
Db 1308 DOLOATQTVINNDONATTEKEKAI-----QOLATA-----VTDANK 1345
OY 825 NVPAYVPLSEYNAVEREKMEAOGNTELPOLGAVVSEELSKTVHTVSVAVIDGTRAVT 884
Db 1346 NITAA---TDDNGVDQAKGAKNSIQSTQPATYKSNAKNDVDQAVTTQNOAIDNTGTAT 1402
OY 885 SVEERSPSMISAVTEPLEHTAGEAMPVEEYTERKDIIEETPVLTQTLPEBGD-AHDM 943
Db 1403 TEE-----KNAKDLVLKAKERAYODILNAOT--TNDVTQIKDAQVADI 1444
OY 944 VISEVDTSEAVTATESETSEALRTEEVTEASGAETTDMYSAV-----SOUTDSPDTEEA 998
Db 1445 OGITADTITIKVAKDELAKRANKOKALLIQTADATTEKEQANOQVDAQIOTGONONIEA 1504
OY 999 TPVOEYVSVLDTTEEBEROTAI--LOAVAADVKVEESQVPATQTVORTSKALEKVEEVE 1056
Db 1505 OSIDVNTA-----KDNAIOAIDPIASTD-VKTNARAEILLTEMQ-----NKITEIL 1550
OY 1057 EDSEVLASKERKDYMKGVQOENGAHLAGSTGATPESLEVPVPTADVDHVAITCOYI 1116
Db 1551 NNNETTNEKGNDI--GVRAYAYERGL-----NNINAAVTTGDDVTTAKDJAQV 1596
OY 1117 KLOQLMEQAV-APESSETLTDESETNGSTPLADSDPTADGTQOD-----ETIDSODSKATA 1170
Db 1597 KYOQLHANVYKPKAGKELDQAAADKKTOI--EOTPNASQOELINDAKQEVDTIELNOAKTN 1654
OY 1171 VROSOVTEEAATAQKEEPSTLPNNVPAOEHEGEBRGDVLPTQOELTAAAVPVLAKTE 1230
Db 1655 VOQSS-TNEYVYNNAVEGAKKI-NAVKTSEYKKD-----ALAKIE 1693
OY 1231 VQOEGVMDLDEKV-----KEOEVEVHSG----- 1256
Db 1694 DAYNAVNVNADNSMSTSEIAEAKOKIAELKOTADONVNOATSKDIDVQIHNDNDIN 1753
OY 1257 ----PNSQKAA-----DYTDESVWGAAGQCEKESTEVOSL----- 1288
Db 1754 DYTIPGKESMTDLYAADOKKNNISADTNATODEKQOAIKOVONVOTALESTINNNGV 1813
OY 1289 -----SLEGBEMETDVEKERETKPE-----QVSEGEQETAPAEHGTGYKPYLTLD 1336
Db 1814 DNGDVDDALTOGKAIDAIOVATVPRKANOAIIEVKAEDTKESIDQSDQ----- 1862
OY 1337 MESSERKALGSLGSPSLPDDDKAGCIVOVOSLDTTYTOTAFAVEK-----VIETV 1389
Db 1863 LPAEETTELAMI---KQITDOAKOGI-----TDATTTAA-VEKAKAGLEAFDNI 1909

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OY 1390 VISETGESEPCVGAHLLPAEKSSATGHWTLQHAEDTVPLG-----PESQAESI 1438
Db 1910 QIDST-----EKOKAIE---ELEFALDOIENGAVNANDATTEKEATNML 1952
OY 1439 PIIVTPAPESTLHPDLOGEISASQRESESEEDKPDGAPDADKESTAIERKVAEPEIL- 1497
Db 1953 EDILSKATEDISQDTNNAELATVKNKSLQDLKAQRINPEVKKNALEAIREVNNKOIEILK 2012
OY 1498 --ELESKNKIYLVNTQTAVDQFARTETAPETHAYOSQV---VPA 1538
Db 2013 MADDASAKEIAFTDGTGRYFDRPADKLDKRTQTNAAVEALQNVTPA 2058

RESULT 12
US-09-919-172-98
; Sequence 98, Application US/09919172
; Patent No. US20020119463A1
; GENERAL INFORMATION:
; APPLICANT: Paris, Mary
; APPLICANT: Turner, Christopher M.
; TITLE OR INVENTION: PROSTATE CANCER MARKERS
; FILE REFERENCE: PA-0036 US
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/222,469
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PERL Program
; SEQ ID NO 98
; LENGTH: 3256
; TYPE: PR
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. US20020119463A1 2700132CD1
US-09-919-172-98

Query Match 4.7%; Score 377; DB 10; Length 3256;
Best Local Similarity 20.2%; Pred. No. 4.9e-09;
Matches 387; Conservative 241; Mismatches 762; Indels 524; Gaps 83;

OY 14 OPAGSDTPESELYLSGH-----GPAEASGAADPDADPATRLPKNGQL 58
Db 1412 QTSGETTHTDKXPGGDKSINAFRETAOKKIDPRASVYTSKRNH-----KTKKQAPL 1464
OY 59 SSYNGVAEOGDVHVOENOGQBE-----EYVEDVGQR--ESDEVREKQVDEM 106
Db 1465 EDLAGKKELEFQTPVCTDKPTTHEKTTKICARSQPPVDPTSSKRSKLKRVDEEERF 1524
OY 107 AANSTVAEDITK-----DGOE-----ETSEIIEQIASENNVDEMOPAES 147
Db 1525 FALRKTPSAGKAMHTPKRAVSGEKNTYAFMGTPVOKLDLTNLGSKRRRLQTPREKQA 1584
OY 148 QANDVGFKKVFYFVGFKFTVKKDKNEKSDPYOLLTVKKDEGGAAS-----VGA 197
Db 1585 LBDLAGFKELFQTRG--HTHEESMTNDKTAKVACKSSQPDLDKNPSSKRLKTLISLKVY 1642
OY 198 GHQEBPSEVTAVGESAKSESLKOSTEKOETLKOQSSTEIPLQAESDQAAEBEAKDEG 257
Db 1643 KEEL-----LAWGKLTQTSGETTHHTTEPTGDKSKAKMESP-----KQIDSAASLIG 1692
OY 258 EKEKEKEPTKSPESPSPYN-----SETTSSFKKFTHGAGGRKTSFPKSKSEDDLETA 313
Db 1693 SKROLRTPKGSEVPDLAAGTLELFOTPSHTKESMTNKT---TVYSYRASQPDVLVPT 1749
OY 314 KRKEQ---EAERVDEEEK-----EKTEPAS-----EEOE-----PAEDTQD- 346
Db 1750 SSKPQKRSLRADNDEEBELARFKQTPSAGKAMHTPKRAVGEKQINTFLGTPVOKLDP 1809
OY 347 -----ARLSADYERKVELPLEDOVDLE-----ASSEK-----CAPLATEVFD 384
Db 1810 GNLPGSNRLQTRKEKAQ--ALEELTGFRLELFOPTDNTPTDEKTTKILCKSPQSDPAD 1868

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QY 385 -----EKEAHOEVVA--EVHVSVEKTEEBOGGGEAGGVVEGTESLP 429
Db 1869 PTLNTRQORPKRSILKADVEEFELAFRLKLPSPAGKAMHTPKAVNGEKDLNTFVGT-----P 1924
QY 430 PEKL-----ABQEVPOBAEPAEELMKSRMCVSGGDHTO-----LTDLS--- 469
Db 1925 VKRLDLGNLPGSKRRPQTPKEKAKALEDLAGFKELFOTPG--HTESMTDDKTTEVSCS 1983
QY 470 --PEEKLPHNEGIVSEVEMLSOERIKVQSP--KFLTSSSLKTLGSKKQKGGK 524
Db 1984 POPDPYKTP-----TSSKORLKLISLGVKVEEVLPGKLTQSGTQTOTHR 2031
QY 525 GGDDEEPGEYOHHTESPESA--DEQKGESSASSPEEP--EETTCLEP-----KGLTAPAD 576
Db 2032 TNGD---GKSIAFKESANQMDLPANYGGMEMWRTPKEEQSLDLGAFKRLFTPTP- 2087
QY 577 GEAEBCSTSDGKKRREGITPMWASFMMVTPKKRVRRP---SESKEEELKYKSAVLS 632
Db 2088 -HTEESTTDDKTTKLACKSP--PPESMDPTSTRRRPKTPLGKRDIVEELSTALKOLQTT 2144
QY 633 -TD-----STVSEMDQEVTV--GEQKPEEPKRVDTSVSEAL----- 669
Db 2145 HTDKVPGDEDKGINVRETPAKQKLDPAASVTSKROPTPKGAQPLEDLGAKELFOTP 2204
QY 670 ICVG-----SSKKRARKASSSDDEGGPRTLGDSHRA-----EASDKKEAGTDVAV-- 715
Db 2205 ICTDKRTTEKTTKLACRSRQDPDPVGTPIIFKQSKSLRKADVEESLALRKRTSVGK 2264
QY 716 -----PASTQODQAQSSSP--EPAGSPSEGCSTWSEFKRLVTPRKSSKLEKAE 768
Db 2265 AMDTPKAGDEKDMKAFMGTQVKLDPGNLPGSKRMPQ-----TPKEAQA--LEDLG 2318
QY 769 DSSVEQLSTEIEPSRESWVSI-----KKFIPRRKKRBDGQKQATVED 813
Db 2319 FRELFOPTGDKTTDEKTTKLACKSPQDPDPTPASTQORPRKRNLRKADVEEFLALRK 2378
QY 814 SGFVELNEDDPNPAVAVPLSEYNA--VER--EKEAOGN-----TELPOLLGAVY 859
Db 2379 RPPSAGKAMDTPKPAVSDKRNITFETPVQKLDLGNLPGSKROQOTPREKALEDLV 2438
QY 860 VSEELSKTLVHYSAVIDGTAVTVSEERSPSWISASTEPLEHTAGEMAPVEEYTEK 919
Db 2439 GKELFQOTGHTESMTD---KITEVSCSP-----QPSFSTSSSKORLKITPV 2487
QY 920 DIIAETPV---LQTLPEGKAHND-----MYTSEVDFTSKAVTATETSEALR 965
Db 2488 KYDMKEEPLAVSKLITSGEOTTOHTPEPTGDSKISAKFESPKQIILDPASAVTGSROLR 2547
QY 966 T-----EVTASGAEE--TTDMVASVSLTDSPTTEATPVQVEESGV 1008
Db 2548 TREKARALEDLVDFKELSPAPGHTESMTIDKNTKIPCKSPPELTDATSTRKCPKTR 2607
QY 1009 LQTEEBERTQALQAVAKVKEESQVPAQYQRTGSKALEVEVEEDSEVLASEKER 1068
Db 2608 LRKEVEE---LSAVERLYQTSQSTHTHKEPASGDEGIKVLRKARKKPNVEEPS 2662
QY 1069 DWMPKQPVQEA--GAELHA---QGSFQGAQTPES-----LEVPVTLADVOH 1109
Db 2663 RRRPRAPKEAOPLEDLAGFTLETSIGHTQESLTAGKATKIPCESPRLLEVYDTTASTKR 2722
QY 1110 VATQVQIKLQOLEQAVAVESSETLTDSSTPLADSDTA----- 1151
Db 2723 HLRTVQKVO---VKEEPSAVKFTQTSGETTDADKEPAGEDKIGALKESAKQTPA 2775
QY 1152 -----DGTQODETI-----DSQSKATAVAAROSQVTEEBA 1182
Db 2776 PAASVTSRRRRPAPRESQAIEDLAGFKDPAPAGHTEESMTDKTKICKSPPELEDTA 2835
QY 1183 TPOKEEPTLPPNVPAQOEHEGEPGRDVLEPTQOELLTAAPVLAKTVEGQSEVDMWLG 1242
Db 2836 TSSKRPRTPRAQKVEVEE-----LLAVGKLTOT---SETTHHTK 2873
```

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QY 1243 EKVKEQEVFVHSGPNQAKAADVTYDSE--VMG-----VACQEKESTE 1284
Db 2874 EPVGECKGTAKFQOPAKRR-----LDAEDVIGSRORPAPRKEAOPLEDLASFOELSQTP 2928
QY 1285 VQSLSEBEME--TDVEKEKRET--KRPVSEGBDEBTAPRHEGIGYKRPVLTLMPSSE 1341
Db 2929 GHTHEELANAAQSFSTAPAPQTPDSCGPLKTS---RVLRAPVVE--PVGQVSTRD--PVKS 2983
QY 1342 RGAALGSLGSPSLPQDQAGCIENVQSLDPTVQOTAP-----AVEKIEFTVISETGE 1396
Db 2984 QSKSNTSL---PLPRKRGG-----KDSVYGTKRLRCMPAPELVEE----- 3024
QY 1397 SPECVGHLLPPEKSSATGSHWTLQHAEDTVPLGPESQAESIPITVTPAPESTLHPDLQ 1456
Db 3025 -----LPASKK-----QVAPRARCKSESPVIMKRSLTRSAKRTEPAE 3063
QY 1457 EISASORERSEEDK--PDGPPADG--KESTALEKVLKAPELLELESKNKIVLVNIOQA 1514
Db 3064 ELNSNDMKTNKEEHKLQDVPENKGISLSRRONKTEAEOQITFEVFLAERIEIN----- 3118
QY 1515 VQOFARTE-----TAPETHAV--DSQOTVPACRLDSREPRRCMTKMKDAKMKHP 1561
Db 3119 -----RNEKKPKMTPSEMDIQNPDDGAKRPTRDKVTENKRLRSARQNESSQP 3167
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RESULT 13
US-09-764-176-7
; Sequence 7, Application US/09764176
; Patent No. US20020127553A1
; GENERAL INFORMATION:
; APPLICANT: NOTEBORN, Mathieu Hubertus Maria
; APPLICANT: DANEN-VAN OORSCHOT, Astrid Adriana Anna Maria
; APPLICANT: ROHN, Jennifer Leigh
; APPLICANT: WEISS, Bertram
; TITLE OF INVENTION: APOPTIN-ASSOCIATING PROTEIN
; FILE REFERENCE: 472508
; CURRENT APPLICATION NUMBER: US/09/764,176
; CURRENT FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 1400
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc. feature
; OTHER INFORMATION: Description of Sequence: Amino acid sequence deduced from the
; OTHER INFORMATION: Ictc acid sequence of AAP-
US-09-764-176-7
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Query Match 4.6%; Score 368; DB 10; Length 1400;
Best Local Similarity 19.6%; Pred. No. 4.6e-09;
Matches 283; Conservative 226; Mismatches 495; Indels 442; Gaps 65;

QY 95 EDVREKRDVEEAMNASTAVEDI--TKDQGETSEIIEQIPASENNVEWVQAPESQANDV 152
Db 92 DNLKFNINIEEDADIMRLQPIGRDKGLMYVQLDO-----DHWVWVYIEQDODDGS- 145
QY 153 GPKKVFYGFQFTYKKDKNEKSDTYQLLTVK-----KDEBGEAEASGADHDQEPSVE 206
Db 146 -----SMKCIV--RNNEELAEITALLKAOIDPVLYLNSSQQDNSS-----RESPLE 190
QY 207 TAVGESAKSESELKOSTEOEGTILKQOJSTELPQOAESDOAAE--EPAKDEGEEOKE 264
Db 191 ----DEETKKEETPKROEBKE---SEKMSSEQPHLEKRNSTANVLEETVYKKKEDEKE 244
QY 265 PTK-----SPESPSPVNSSETTSFKKFTHGAWGMRKTSFKKSKEDDLET--- 311
Db 245 LVKLPIVTLKPLPENNEKKIIEESDSFKENVK-----PIKVEVKCRADPKDTKSS 298
QY 312 AEKRKEQAEKXD-----EEKEKTEPASEQOPADDTQA-----RLSADYE--- 354
Db 299 MEKPAQOEPRIEFGNIKSSHEITEKSTETEKLNQOAKIPIPKKREIKLSDDFDSPV 358
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[illegible]

QY	1196	VPADEHGECEPRDVL	----	SEPTOO	-----	ELTAAAVPVLAKTEVSGEGEDWLDGSKV	1245
Db	1331	-----NGOSPEKAIENTLIGKFTKSTQTPKDNSTASLASNGTSGGDEA	-----	GAPE	1378		
QY	1246	KEEOEV	1251				
Db	1379	EDEEDL	1384				
RESULT 14							
	US-09-963-875-1						
	Sequence 1, Application US/09963875						
	Patent No. US20020164307A1						
	GENERAL INFORMATION:						
	APPLICANT: Massachusetts General Hospital						
	TITLE OF INVENTION: Stem Cells of the Islets of Langerhans and Their Use in Treating						
	TITLE OF INVENTION: Mellitus						
	FILE REFERENCE: 17633/1235						
	CURRENT APPLICATION NUMBER: US/09/963,875						
	CURRENT FILING DATE: 2001-09-26						
	PRIOR APPLICATION NUMBER: US60/169082						
	PRIOR FILING DATE: 1999-12-06						
	PRIOR APPLICATION NUMBER: US 60/215109						
	PRIOR FILING DATE: 2000-06-28						
	PRIOR APPLICATION NUMBER: US 60/238880						
	PRIOR FILING DATE: 2000-10-06						
	PRIOR APPLICATION NUMBER: US 09/731261						
	PRIOR FILING DATE: 2000-12-06						
	NUMBER OF SEQ ID NOS: 58						
	SOFTWARE: PatentIn version 3.1						
	SEQ ID NO 1						
	LENGTH: 1618						
	TYPE: PRT						
	ORGANISM: Homo sapiens						
	US-09-963-875-1						
QY	Query Match	4.4%	Score 354;	DB 9;	Length 1618;		
	Best Local Similarity	20.1%	Pred. No. 2.2e+08;				
	Matches 342;	Conservative 224;	Mismatches 623;	Indels 510;	Gaps 75;		
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QY	224	EKOEGT	-----	LKOBOSSTREI	-----	PIQAE	-----
Db	86	ELBEVAGRCQELRLARERTTEEVARNRRAYAEKCARAWLSSQCAELERLEMLRVANHE	145				
QY	257	-----GEEKOEKPEPKSPSPSSPVNSETTSSEKFFTHGAG	-----	WRKTSFKK	303		
Db	146	EEVGLINQAACAPRLPAPRPAPAPAVEELARLGEAMGAVNGYQERYVAHHNETSLDQ	205				
QY	304	SKEDOLETAEKRKE	-----	QAEKVDEEEKTEKTPASDEQEPADTQARLSAYEVEVLEPL	361		
Db	206	TREIRARVQAGARERLLOQLQDAERGGLLERRALLEQRLGRMQRIRAR	EFQOLAVE	264			
QY	362	DOVGDLEASSEKCAPLATEVFEDEKMEAHQVVAEVHST	-----	VEKTEEOGGG	--	413	
Db	265	-----ALBEKCGLOSQIAQVLEGRQOLAHKMSLSLEVATRTLLAEANSRLQTPGGGSK	320				
QY	414	-----BAEGGVVEG	-----	TGESP	---	PEKLAEPQEVPOEAE	PAEELMKSRMCV
Db	321	TLSLSDPEKLELOPFRTPPEGRRRLGSLPLVLSPTSL	---	PSPLPATLETPVP	PAFLKNQEFIQ	378	
QY	458	SGGHOTQTLDSPEKTLPKHREGEVSEVEMLSQERKKNVQSPPLKTLFSSSGLKLSGK	517				
Db	379	AKPTPLASTPIPP	---	TPQAPSPAV	-----	DAETIRADAPISLTQITGGKQAP	426
QY	518	KOKGRG	-----	GDPEP	---	GEYOHINT	ESPESADBOKESSASSPEDEETTCLEKG
Db	427	LRAERVAIPASVLRGPREFPGGQROEASTGSPED	-----	HASTAPPLSDHSS	-----	475	
QY	570	PLEAPDGEAEAGETT	-----	SDGEKKREGITP	-----	WASKFKWTPKKKVRPSE	615

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Db 476 -LEA-KDSESGSVFYSICRGEGEIOIMGLVERETAIEKVVSSLOQELWEEDLNKKEI 533
Qy 616 SKEEELKVKATLSSTDSOTVSEMODEKKTWGE-----EOKPEPKRVRVTSVMEAL 669
Db 534 QDSQVPLEK---ETLKSIG---EEIOESLKTLENOSSHETLEENOCPSRLSEDL--ETL 585
Qy 670 ICVGSKKRARRKASSSDDEGPR-----TLGDSHRAEASKDEA----- 710
Db 586 KSLKENKRAIGCGSESRKRGCGQLKPTGKEPTQITQSLQKKNQMLKSLGULETF 645
Qy 711 ---GTD--AVPASTQEDQ---AQSSSPPEPAGSPSEEGV----- 744
Db 646 LPPGTEMOELVSLQENLESLTALKEKENOEPLRSPVGEALRPLTKENOEPLRSLDE 705
Qy 745 TWSEFRVLTTPRKKSKEEKAEDSVFQSLSTE-----TEPSRESWTSIKKPIPR 797
Db 706 NKEARSLKEKOEPLKTLKEE--DOSIVRPLETENHKSRLSEBODQETLRTLEK--ETQ 762
Qy 798 RKRADGKOQATVEDSGFVEINEDDPNVPVAVPLSEYNAVEREKMEAQNTLPQLGA 857
Db 763 QRRLSGEDQMTLRP-----PEKYDLEPLKSLQD----- 793
Qy 858 VYVSELSKTLVHTVSVAVIDGRAVTSVERNSPWSIASVTEPLEHTGEMAPPEVYT 917
Db 794 -----IARPLENQEFLKSLKEES 813
Qy 918 EKDIIAETPVLITQLPEKDAHDMVTSEVDTSEAVTATENSEALRTVEYTEASGAE 977
Db 814 VEAVSLEETLEILSKSAGOE-----NLETLSPETOAPLWMTPEELINKSGME 861
Qy 978 TTDWMSAVSOLTSDPDTEATPVQEVESGVL-----TEEE 1014
Db 862 SSRKGSRTTGVCGSPRIQPPRG--ESGIIISGSMPEGEFISRGVDEKQSLKEE 920
Qy 1015 ERQTOAILDADVAKVEEQ--VPATQTVQRTGSKALEKEVEVEDEY--LASKEDQVMP 1072
Db 921 ENLKEGEYESLRLSEEOELPQSDAYOR--WEDYVEKQOELAQESPPGAGVEND-- 976
Qy 1073 KGPVOAGAENLAQSETGOATPESLEVEPVYADVD-----HVATCOYIKLOOLMEQA 1125
Db 977 -----EAILNLRBQDGFTR--EEVYEGELNATEEVMFPGEBHPNPEKRGILVEGA 1029
Qy 1126 VAPESSETLTDETSNGS-----TPLADSDTADGTQ---DETIDSODS 1165
Db 1030 SVKGAEGLODPEGSOQYGTPLQAPQGLPEALIEPLVEDVAPRGDDQASPEVMLSSEA 1089
Qy 1166 KATAV-----ROSQVTEERATPAQKEPESTLPNNVAQE----- 1200
Db 1090 MGESASAGAPGLQGVGGLDPRGLHTRREVMERPLEEESLEAKRQGLDGRPKDLEBAG 1149
Qy 1201 ---EHGEERG--RDVLEPTQO---ELTA---AAVPLAKTEVGOBEVWMLGEEKY 1245
Db 1150 LGTEFSELFGKSDPPEPRREGRESEEARPRGAERAPAEITIGHGSDAPSPWPLGSEE 1209
Qy 1246 KEEO-----EYFVHSGPNSQAKADVTYDSEVMGACQOKESTEVOSLSLEEG 1293
Db 1210 AEDVDVPLVSPSTYTPILEDAPGLQPOAEGSOEAS--WGVOARABAGKVESBOELGSG 1268
Qy 1294 EMETDVEKREKREKPVQVSEEGQETAARBEH--GTYYGK-----PVLTLDMPSESG 1343
Db 1269 ELPEGLQEGEESRE--SEEDELGETLPDSTPLGFLYLSPTSPRMTPLRESRHPKLEKG 1326
Qy 1344 K-----ALGSLG--GSPSLPDODKAG---C-----IEVOQSLDTVT---OTAEA 1381
Db 1327 KEGMDPAVVLASEGLEPSEKEGEBEGEGRSDLSSEEDULGTAPPLPGVPGEYAE 1386
Qy 1382 VEKVETVV-----ISETGESPE-----CVGAHLPL 1407
Db 1387 LGQVPLLLDPAAMDRDSDGFADEEESGEEBEGQEGREHGAGRWPGSSVGS--LQ 1444
Qy 1408 AEKSSATGGHMTLQHAEDVPLPGPESQAESIPITVPAPBSTIHPDLQ--GEISASORER 1465
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Db 1445 AUISSORGEFLESVSVPWD-----DSLKGAVAGAPKTALETESODSAEPSCSEERS 1499
Qy 1466 S-----EEDK-----PDAGPDADGKESTAIIEKYAKAPELLELSKSNKI---V 1507
Db 1500 DVSLEIREKVKGPLEIPSGMEDAGPAD-----IIGVNGGPNNEGKSHVNGCV 1550
Qy 1508 LNVIGTAVDQFARTETAPE 1526
Db 1551 MNGLEQSEESGARNAIYSE 1569

RESULT 15
US-09-864-761-36182
; Sequence 36182, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: Aecmics-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 36182
; LENGTH: 617
; TYPE: prt
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC005529.7
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 0.94
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
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